В Ş В Ş 밁 Š Query Match 7.2%; Best Local Similarity 23.8%; Matches 35; Conservative 17 161 ---IRMTFD-----TWKSFTDF 174 127 DSSVVPTFELTLVFKQENCSWTSFRDF 153 140 KEK------67 KSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRIVC 126 | :|:|||| | 88 PFNITELLDNIVSLTTAESESFVLDF------PQPSADYLDFRNRLQTNHV-CLENCVL 139 12 PASISELLD-----CGYHPESLLSDFDYWDYVVPEPNLNEVIFEESTCONLVKMLENCLS 66 12; ------AIAGTVKVQNLAFEKVVK-----Score 72.5; DB 2; Length 284; Pred. No. 1.3; Mismatches 35; Indels 65; Gaps

LENGTH: 284
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-480-203-3 NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3 APPLICANT: Philip Cohen
APPLICANT: Peter R. Young
TITLE OF INVENTION: A PROTEIN PHOSPHATASE 1 BINDING PROTEIN
TITLE OF INVENTION: RS
TILE REFERENCE: ATC-50033-2
CURRENT FILING DATE: 2000-01-10
EARLIER APPLICATION NUMBER: 09/300,327
EARLIER APPLICATION NUMBER: 09/300,327
EARLIER FILING DATE: 1999-04-27
EARLIER FILING DATE: 1999-04-27
EARLIER FILING DATE: 1999-04-27
EARLIER FILING DATE: 1999-04-27 GENERAL INFORMATION: Sequence 3, Application US/09480203 Patent No. 6297359 EARLIER APPLICATION NUMBER: 08/767,096 -09-480-203-3 APPLICANT: Patricia T.W. Cohen 1996-12-05

Query Match Best Local Similarity 7.2%; 23.8%; Score 72.5; DB 4; Length 284; Pred. No. 1.3;

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48 --IFEESTCQNL-VKMLENCLSK-----

401 PEDISELL----HSITLLAHLT-GDTVIQGSATSLRAPPEPADSLTEACRQYGRETLAYL 455

-----SKQTKLG-----CSKVLVPEK 83

12 PASISELLDCGYHPESLLSDFDYWDYVV------PEP--NLNEV----

US-09-085-199B-9

ORGANISM: mouse

FEATURE:
OTHER INFORMATION: Huntington-interacting protein

Matches 49.

Query Match Best Local 9

Match 7.2%; Local Similarity 24.5%;

Conservative

22;

Mismatches

71;

Indels

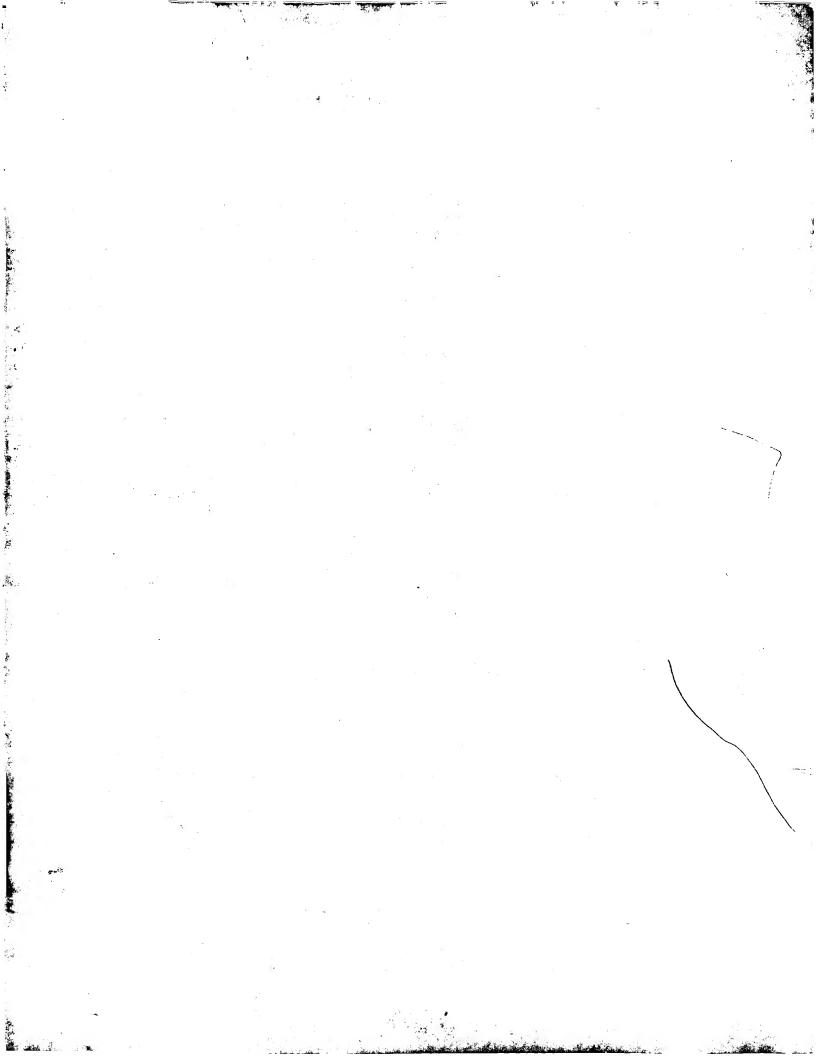
58; ----- 47 Gaps

10;

Score 72; DB 4; Length 756; Pred. No. 6.4;

ppedahl 6 La ox 5270 270 LE FORM: Diskette, 3 Diskette, 3 M Compatible FEM: MS DOS GOPETFOR TION DATA: DMBER: US/05 V: UMBER: 3202 V: UMBER	DE ADDRESS: Oppedahl & Larson	E ADDRESS: E ADDRESS: Oppedahl & Larson Oppedahl & Larson Oppedahl & Larson Oppedahl & Larson Oppedahl & Larson Oppedahl & Larson Occo DOX 5270 E DOX 5270 CC DOX 527	DADRESS: 44 DADRESS: ADDRESS: Oppedahl & Larson Box 5270 Box 5270 ABLE FORM: ID Iskette, 3.50 inch, 1.44 Kb s IBM Compatible VSTEN: MS DOS 5.0 WOODEPER: MS DOS 5.0 WOODER: US/09/085,199B ION: INFORMATION: ON, Marina T. NUMBER: 32038 NUMBER: 32038 OKET NUMBER: UBC.P-013US2 PION INFORMATION: (970) 668-2052 SEQ ID NO: 9: COTERISTICS: ACTERISTICS: COTERISTICS: CE: E: E: E: E: Oppedahl & Larson A Kb Larson B Larson A Kb Larson B Larson A Kb Larson A Kb Larson A Kb Larson B Larson A Kb Larson A Kb Larson B Larson A Kb Larson A K	COPECADA LAISON OPPEDAIL & LAI	DADRESS: 44 DEDRESS: 94 DADRESS: Oppedahl & Larson Box 5270 E ADDRESS: Oppedahl & Larson Box 5270 CO CO CO CO CO CO CO CO CO C
Oppedani 6 La Oppedani 6 La Oppedani 6 La Oppedani 6 La Sax Sax ABLE FORM: I Diskette, 3 IBM Compatible YSTEM: MS DOS WOYDER Fect CATION DATA: NUMBER: US/0; ION: INFORMATION: ION: INFORMATION: ON NUMBER: US/0; ION: ON NU	Oppedahl & Larson) Box 5270 CCO CCO CCO CCO CCO CCO CCO C	Oppedahl & Larson) Box 5270 CCO CCO ABLE FORM: ID Iskette, 3.50 inch, 1.44 Kb s IBM Compatible YSTEM: MS DOS 5.0 WORDER: US/09/085,199B : ION: T INFORMATION: ON, MARINA T. NUMBER: UBC.P-013US2 PTON INFORMATION: (970) 668-2052 SEQ ID NO: 9: SEQ ID NO: 9: CCTERISTICS: D acid Linear Inportein INPORTERISTICS: E protein INPORTERISTICS: Protein INPORTERISTICS: Acid	Oppedahl & Larson) Box 5270 CCO CCO CCO CCO CCO CCO CCO CCO CCO CC	Oppedahl & Larson Box 5270 -5270 -5270 -5270 CCO CO CO CO CO CO CO CO CO	Oppedahl & Larson Box 5270 CO CO ABLE FORM: Diskette, 3.50 inch, 1.44 Kb s IBM Compatible YSTEM: MS DOS 5.0 WORDER: US/09/085,1998 ION: T INFORMATION: NUMBER: 32038 COCKET NUMBER: UBC.P-013US2 PION INFORMATION: NUMBER: 9: 100: 9:
.99I	1.44 Kb	1.44 Kb s	1.44 Kb s	1.44 Kb s	1.44 Kb s

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: sp_bacteria:
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6: sp_mammal:*
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8: sp_organel!
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
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14: sp_unclass
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Q9hQ3 homo sapien
Q9hQ3 homo sapien
Q9hX09 homo sapien
Q9d3f7 mus musculu
Q9hhh5 drosophila
Q9vth4 drosophila
Q9vth4 drosophila
Q9vth4 drosophila
Q9vth4 drosophila
Q9vth4 drosophila
Q9th97 arabidopsis
Q76d11 caenorhabdi
Q9dh12 yaba-like d
Q9lh98 arabidopsis
Q76649 caenorhabdi
Q97fz3 clostridium
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ALIGNMENTS

RESULT 1 Q96D03 A I

Qy 121 LDRIVCDSSVVPTFELTL	Qy 1 MVATGSLSSKNPASISEL Db 1 MVATGSLSSKNPASISEL Db 1 LENCLSKSKOTKLGCSKV Qy 61 LENCLSKSKOTKLGCSKV	Query Match Best Local Similarity 100 Matches 193; Conservative	RA Strausberg R.; RL Submitted (SEP-2001) to DR EMBL; BC013592; AAH1359 SQ SEQUENCE 193 AA; 217			ID Q96D03 PRELIMINARY;
LDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRLVKKK	WVATGSLSSKNPASISELLDCGYHPESLLSDFDYWDYVVPEPNLNEVIFEESTCQNLVKM 	100.0%; Score 1002; DB 4; Length 193; 100.0%; Pred. No. 3.8e-96; Length 193; Live 0; Mismatches 0; Indels 0;	Strausberg R.; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013592; AAH13592.1; SEQUENCE 193 AA; 21740 MW; 3BEEB3D0530C5BFF CRC64;	ordata; Craniata; Vertebrata; Euteleostomi; imates; Catarrhini; Hominidae; Homo.	. 19, Created) . 19, Last sequence update) . 19, Last anotation update) 1700037B15 GENE.	r; PRT; 193 AA.
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubi F., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 178
Q9HOS3;
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01-MAR-2001
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01-JUN-2001 (TIEMBLrel. 17, Last annotation updat
1700108M02RIK PROTEIN (1700037B15RIK PROTEIN).
1700108M02RIK OR 1700037B15RIK.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MGI:1925887; 1700108M02Rik.
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01-OCT-2000 (TrEMBLrel. 15, Created)

01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

CDNA FLJ20500 FIS, CLONE KAT09159 (HYPOTHETICAL 25.4
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"Towards a Catalog of Human Genes and Proteins: Sequencing ar Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
EMBL; AL13668; CAB6603.1; -.
                                   Strausberg R;
Submitted (MAY-2001) to the
EMBL; AK000507; BAA91214.1;
EMBL; BC015236; AAH15236.1;
EMBL; BC007714; AAH07714.1;
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PROTEIN).
Homo sapiens (Human).
Homo sapiens (Human).
'Toria; Metazoa; Chordata; 'Arria; Primates;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Suzuki Y., Obayashi M., Nishi
Nakamura Y., Isogai T., Sugan
"NEDO human cDNA sequencing pi
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MEDLINE=21154917;
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Nishi T., Shibahara T., Tanaka
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo: S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo: S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Hofmann M., Carninci P., da Bonaldo M.F.,
RA Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Istorch K.-F.,
RA Mayashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mus musculus (MOUSE).
Eukaryota; Metazoa; Chordata;
Eukaryota; Futheria; Rodentia;
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MEDLINE-21085660; PubMed-11217851;
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LRLSSTEPCGLRGCVMHVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRD
                                                       YLDGVSLPDFELLSDPEDEHLCANLMQLLQESLSQARLGSRRPARLLMPSQLVSQVGKEL
                                                                                                              YWDYV-VPEPNLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLTQRIAQDV
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Pred. No. 3.3e
45; Mismatches
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Pred. No. 3.9e-20;
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Sciurognathi; Muridae;
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O1-MAY-2000 (TrEMBLrel. 13, Cre
T 01-MR-2001 (TrEMBLrel. 16, Las
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CHARYBDE PROTEIN (LD22381P).
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Best Local
SEQUENCE:
STRAIN-BERKELEY;
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J., Adams M.D., Celniker S.E., Li P. W., Hoskins R.A., Galle Amanatides P.G., Scherer S.E., Li P. W., Hoskins R.A., Lewis S.E., Richards S., Ashburner M., Henderso George R.A., Lewis S.E., Richards S., Ashburner M., Henderso Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The second section of charybde and scylla, two of Hox and cofactors proteins in Drosophila."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ (EMBL; AF221109; AAF59840.1; TlyBase; FBgn0036165; charybde. SEQUENCE 299 AA; 32133 MW:
                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Mectazoa; Arthropoda; Tracheata; He
Eterryota; Neoptera; Endopteryota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                SEQUENCE FROM
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CHARYBDE.
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51; Conserv
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Pred. No. 8e-14;
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Chen L.X.,
                                                                                                                                                                                                                                                                                                                                  Insecta
                                            Pfeiffer B.D.
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                                                                                                                                                                                                                                                                                                         Muscomorpha;
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RESULT
Q9VTH4
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RA Baeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Downes P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Correll J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Raizzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Raizzolo M., Siden-Kiamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupskin M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Weinscok G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinscok G.M., Weissenbach J.,
RA Yeinsen S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ph. C., Ph. C., Scheeler F., Shen H., Wang S., Yao Q
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Best Local S
Matches 51
                                                                             Q9VTH4;
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farsfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Vu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB00354; AAF50060.2; -.
EMBL; AY060367; AAL25406.1; -.
           01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16, CG7590 PROTEIN.
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldv
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                                                                                                                                                                                                                                                                                                                                        NLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCG 102
                                                                                                                                                                                               SGFRRTLILSSGFRLVKKKLYS
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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 CG7590
                                                                                              PRELIMINARY;
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                            Last sequence update)
Last annotation update)
                                                                                              PRT;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botchier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nixon K., Supski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Shong F. N., Shong F. N., Pacleb J.M.,
RA Wang Z.-Y., Wassarman D.A., Weissenbach J.,
RA Wang Z.-Y., Massarman D.A., Weissenbach
                                                                                                                                                                                                      RESULT
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Q9NHN4;
01-OCT-2000
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49; Conserv
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                                                                                                      PRELIMINARY;
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Pred. No. 6.1e-12;
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01-MAY-2000
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01-MAR-2001
SCYLLA.
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of charybde and scylla, two paralogous of HOx and cofactors proteins in Drosophila."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases: EMBL; AF221110; AAF59841.1; -. FlyBase; FBgn0041094; scylla.
SEQUENCE 280 AA; 30772 MW; 8B27BC184CD14E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                           Yaba virus."
J. Gen. Viro
                                                                                                                             MEDLINE=95248279; PubMed=7730796; Amano H., Ueda Y., Miyamura T.; "Identification and characterizat
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                 Amano H., Morikawa S.
"Nucleotide sequence
Submitted (JUN-1998)
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Yatapoxvirus.
                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCYLLA OR CG7590
 354
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                                                                                   Gen. Viroi. 76:1109-1115(1995).
BL; AB015885; BAA88814.1; -.
QUENCE 902 AA; 102862 MW; ED
                     سر
                 MVATGSLSSKNPASISELLDCGYHPESLLSDFDYWDYVVPEPNLNEVIFEESTC-----
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 MLAKKSRSKELKSKLSLFWD-
                                                                                                                                                                                                                                                                                                                                                                                                                          VFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRLVKKKLYSLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIE-NVCKKLDRIVCDSSVVPTFELTL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Conserv
                                                    Similarity
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                                                                                                                              characterization
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to the
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21.6%;
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16,
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                                                                                                                                                                                                                                                           RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Mismatches
                                                                                                                                                                                 Y., Miyamura T.;
central 50kbp region of Yaba
EMBL/GenBank/DDBJ databases.
                                      Score 91; DB Pred. No. 1; 41; Mismatches
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Last
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Pred. No. 2e-11;
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                                                                                   ED4373030A2BCF31 CRC64;
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GMDYQEY -- ROKKLSDIIFYNSTCYVMGLY 401
                                                                                                                                of.
                                                                                                                                                                                                                                                                                                                                                902
                                                                                                                                                                                                                                                            Poxviridae;
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a; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                    update)
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                                         73;
                                                            Length 902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 280;
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                                         Indels
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                                         68;
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RESULT 12 076411

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PRELIMINARY;

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01-NOV-1998 (TREMBLIEL 08, 01-NOV-1998 (TREMBLIEL 08, 01-DEC-2001 (TREMBLIEL 19,

Created)
Last sequence
Last annotation

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update) on update)

HYPOTHETICAL 160.1 KDA PROTEIN.

Caenorhabditis elegans. Eukaryota; Metazoa; Nemat Rhabditidae; Peloderinae;

Nematoda; Chromadorea; cinae; Caenorhabditis.

Rhabditida;

Rhabditoidea;

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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,044,082 bp covered physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
EMBL; AB006705; BAB09502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-COLLMBIA;
STRAIN-COLLMBIA;
MEDLINE-98069011; PubMed-9405937;
MEDLINE-98069011; Vakamura Y., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FN97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thallana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eueurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, TRANSPOSON PROTEIN-LIKE.
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651
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DLPGRKLTGMKSHDCHVLMQRLFPIAFAELMDKS
                                                                                                   LHLTPE-
                                                                                                                                                                                                                                                                                                           ILTGEELYNEVCCLPKTVDCGGNHGRLEGYGKTHNWHKQSILWELSYWKDLKLRHNLDVM
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                                                                                                                                                  MHVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSS----
                                                                                                                                                                                                       HIEKNYLDNFIKTLLNVQGKTKDNIKS-----
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                              -GFRRTLILSSGFRLVKKKLYSLIGTTVIEGS
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1089 AA; 126629 MW; 1
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                                                                                                   -GKAPIPKFRLKPDAKEIFLRWLE-KDVKFSDGYSSSLANCV
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Last sequence update)
Last annotation updat
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Pred.
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Matches 46
                                                              Q9DHL2; PRELIMINARY;
Q9DHL2;
01-MAR-2001 (TIEMBLIEL 1
01-MAR-2001 (TIEMBLIEL 1
01-DEC-2001 (TIEMBLIEL 1
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                   101L.
Yaba-like disease virus
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50068; LDLRA_2; 1.

PROSITE; PS50060; MAM_2; 1.

PROSITE; PS50010; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-2001) to the EMBL; AF067949; AAC19236.1; HSSP; P11362; 1FGK.
  Yatapoxvirus.
NCBI_TaxID=132475;
                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Glycoprotein; Hypothetical protein; Tyrosine-protein kinase.
SEQUENCE 1414 AA; 160101 MW; 43800DFE3D48ACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00192; LDLa; 1.
SMART; SM00219; TYTKC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology. The C
Science 282:2012-2018(1998).
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MEDLINE-99069613; PubMed-9851916
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[1]
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investigating biology. The C. ele
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                                                                                                                                                                                                                                                                        LENCLSKSKQTKLGCSKVLV----PEKLTQRIAQDVL-RLSSTEPCG-----LRGCVM
                                                                                                                                                                                                                                                                                            SDEMDCG-NINGTMCDFNGQDYCNSWYQVTNVTDYHERLSEPTTVAPLNKLNEVPLHLFR
                                                                                                                                                                                     FSSGFRRTLILSSGF
                                                                                                                                                                                                          RFYLCSRTYSKVWQISVISKGINPMESGRTIIYEAGYTLIPK-ENCTW---ERVFVNIPR
                                                                                                                                                                                                                                                   LQSPSAKIKEAMRGSGNMLVFDHKPNPLTRRTSALVSPELPRTNPEAYDEKSPLFKSCKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                        46;
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; IPROUZ998; MAM.
; IPROUZ45; Tyr_pkinase.
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IPR002172; LDL_recept_A.
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                       -EIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGR
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23.6%;
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egans cosmid T10H9.";
o the EMBL/GenBank/DDBJ
                      (YLDV)
                                                                 16,
19,
                                                                                                                                                                                                                                                                                                                                       35;
                        RNA
                                                                                                                                                                                                                                                                                                                                     Score 85.5; DI
Pred. No. 6.4;
35; Mismatches
                                                                 Created)
Last sequence update)
Last annotation updat
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                                                                                                           PRT;
                       stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans: a platform
ns Sequencing Consort
                                                                                                           902
                       Poxviridae; Chordopoxvirinae;
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                                                                 update)
                                                                                                                                                                                                                                                                                                                                      73;
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DCT-2000 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, BAC CLONE: T19N8.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21176366; Pub
Lee H.J., Essani K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (2000), Sir
EMBL; AJ293568; CAC
SEQUENCE 902 AA;
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                                                     EMBL;
                                                             TAC and BAC clones. TDNA Res. 7:217-221(2)
                                                                            Sequence features of TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                   Q9LH98
                                            SEQUENCE
                                                                                                                       MEDLINE=20363099; PubMed=10907853;
                                                                                                                                  STRAIN-COLUMBIA;
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                  Submitted (MAY-2000)
                                                                                                                                                                             Kaneko
                                                                                                                                                                                       STRAIN-COLUMBIA;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE FROM
                                                                                                  "Structural analysis
                                                                                                            Nakamura
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                                          es. 7:217-221(2000)
AP002057; BAB03174.
NCE 2081 AA; 2328
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47; Conserv
 30;
           Similarity
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; CAC21339.1; -.
AA; 103042 MW;
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                                                                                                                                                                  , Nakamura Y., Asan
EMBL/GenBank/DDBJ
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Pred. No. 5.3;
44; Mismatches
Score 82.5; D
Pred. No. 21;
l3; Mismatches
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No. 21;
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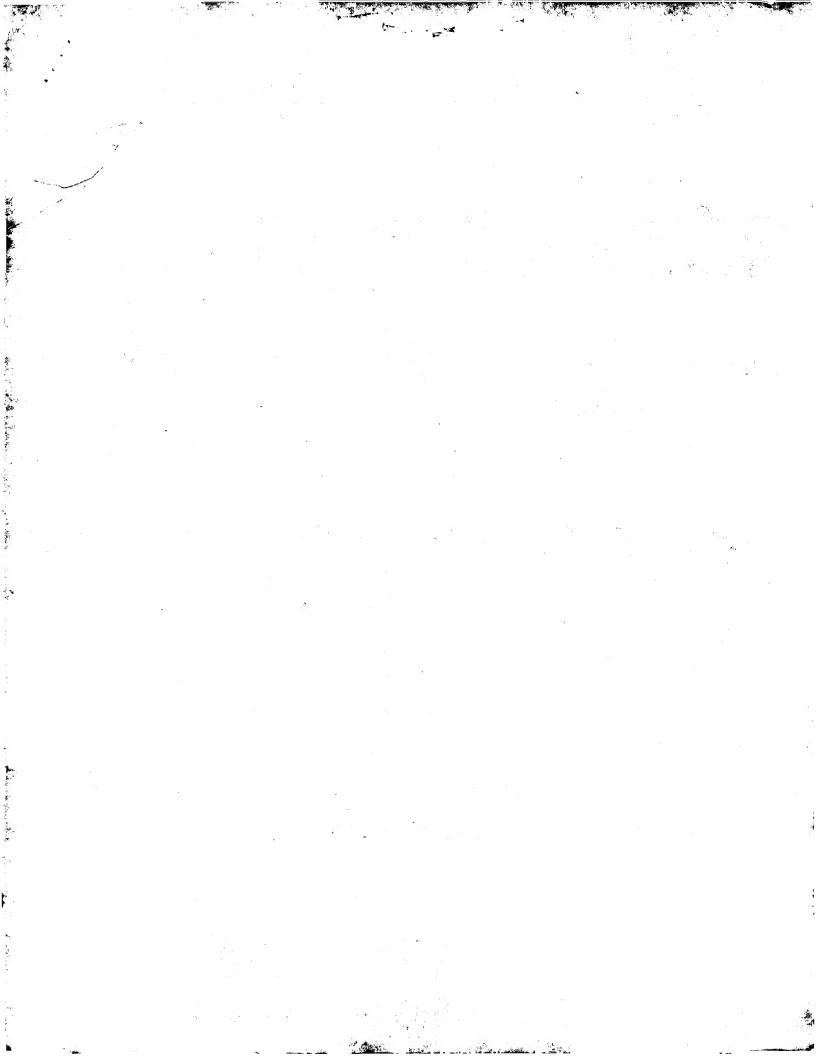
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LEIENVC

KKLDRIVCDSSVVP--

TFELTLVFKQENCSWTSFRD

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RESULT 15
076649
ID 07664
AC 07664
DT 01-NC
DT 0
Search completed: October 11, Job time : 92 secs
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Best Local S
Matches 29
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF078157; AAG24078.1; -
InterPro; IPR0001254; BTB_POZ.
InterPro; IPR001254; Trypsin.
SMART; SM00225; BTB; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS50097; BTB; 1.
Hydrolase; Hypothetical protein; Serine protease.
SEQUENCE 673 AA; 77122 MW; 8ED29BE157C9D8C7 CRC64;
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O76649;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 77.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Wilson R., Bradshaw H.;
"The sequence of C. elegans
Submitted (JUL-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
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STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                       LARGRINTADPYILEDITPIDFKLYMDLTYHPKQYFSAYHAKDILQIAKRFNNLEVV--- 241
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l Similarity 26.9%;
29; Conservative 2
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                            2002, 14:13:46
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%; Pred. No. 6;
21; Mismatches
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EMBL/GenBank/DDBJ databases.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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     /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Packfiles1.pep:*
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US-08-781-891-78
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US-08-325-071-96-3
US-09-4860-203-3
US-09-085-199B-9
US-08-325-071-56
US-08-461-004A-56
US-08-461-004A-57
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US-08-461-004A-57
US-08-954-418-2
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US-08-325-071-15-7
US-08-325-071-63
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                 Query Match
Best Local Similarity
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6.6	6.6	6.7	6.7	6.7	6.7	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9
1023	1023	257	613	613	613	3079	650	650	620	620	542	481	280	280	280	280	739
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US-08-870-693-4	US-08-198-446B-4	US-08-981-256A-12	PCT-US94-11843-2	US-09-030-970-2	US-08-465-687A-2	PCT-US94-00198-4	US-08-461-004A-67	US-08-325-071-67	US-08-461-004A-65	US-08-325-071-65	US-08-959-381A-2	US-08-959-381A-1	PCT-US93-05651-3	US-09-234-186-3	US-08-471-057-19	US-08-471-058-19	US-08-836-943-2
Sequence 4, Appli	Sequence 4, Appli	Sequence 12, Appl		Sequence 2, Appli	Sequence 2, Appli	4, 2	•	Sequence 67, Appl	•	Sequence 65, Appl	Sequence 2, Appli		Sequence 3, Appli	3, ,	•	Sequence 19, Appl	Sequence 2, Appli

ALIGNMENTS

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US-08-576-626A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/08576626A Patent No. 5998194 GENERAL INFORMATION:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 587.U
TELECOMMUNICATION:
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,6:
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
                                                                       STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                         No. 5998194e
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8.4%;
22.2%;
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Score 84;
Pred. No.
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DB 2;
0.051;
                   Length 286
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US-08-559-303B-78
; Sequence 78, Application US/08559303B
; Patent No. 5824501
; GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES
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PCT-US93-05701-2
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                                                                                         RESULT 3
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.9%;
Best Local Similarity 24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Massachusetts Institute of Technology TITLE OF INVENTION: Cloning and Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                       10 KNPASISELLD-CGYHPESLLSDF--DYWDYVVPEPNLNE--VIFEESTCQNLVKMLENC : : | : | | : | | : | | | | : : | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: POFILING DATE: 19930614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 02139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                        ---DRKLLLG----NVPKQMT-----CYIR-----EYHVDRVIKKLD--
                                                                                                                                                                                                                                                                                            LSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRI 124
                                                                                                                                                                                                                                                                                                                                   RQASELGPLIDFFNYNNQSHLADFLEDYIDFAINEPDLLRPVVIAPQFSRQML-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTKLSIPEVILFEPRIFEDDRGHFFESFNLAKFQESIGRQVTFVQSNESYSKQNVIRGLH 62
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                                                                                                                                          181
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amino acid
GY: linear
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        NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
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                                                                                                                                                                                                       EMCDLDSF--FLFLHGRAGSG--KSVIASQAL----SKSDQL 179
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Pred. No. 0.55;
23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                     115
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                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                               Sequence 78, Application 5-08-701 No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,303B
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                      APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 63: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ME
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                      APPLICANT:
                                        CORRESPONDENCE ADDRESS:
                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                    349 SM---QELNPETSTDCDARQISLQQQLIHV---MEHICKLIDTIPDD 389
                                                                                                                                                                                                                                                                                                                                                                      293 DDDYDTDFVPPSP--EEIISASSSSSKCLSTLKDLDT--SDRKEDVLSTSKDLLSKPEKM 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID STRANDEDNESS: SII TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                     85 TQRIAQDVLRLSSTE----PCGLRGCVMHVNLEIENVCKKLDRIVCD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                           ADDRESSEE:
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34; Conserv
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NEW YORK
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                                                                                                                                                                                                                     Application US/08781891
                                                                                                                                    Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
          6300
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     SEED and BERRY LLP
00 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6221643
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NATHAN A.
APPLICANT: GRODEN
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
                                           FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1417 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 SM---QELNPETSTDCDARQISLQQQLIHV---MEHICKLIDTIPDD 389
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                                                                                                               FILING DATE:
                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 TQRIAQDVLRLSSTE----PCGLRGCVMHVNLEIENVCKKLDRIVCD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                             ELIZABETH A. BOGOSIAN
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                                                                                                                                                                                                                                                                                NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09175828
                                                                                                                                                                                                                                                                                                                 90 PARK AVENUE
                                                                                                                                                                                                                                                              U.S.A.
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NO: 78:
NUMBER:
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                                                                                                                                                                                MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                                                                                ROTHSTEIN & EBENSTEIN
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                                                                          us/08/559,303
                                                                                                                               us/09/175,828
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63475/65
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Pred. No.
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Patent No.
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TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 17-MAY-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                           FILING DATE: 07-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                  STREET: 3000 K SLI
CITY: Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
                                                                                                                                           APPLICATION NUMBER: US/08/325,071 FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 DFDY-WDYVVPEPNLNEVIFEEST----CQNLVKMLENCLSKSKQTKLGCSKVLV--PEKL 84
                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: OTHER INFORMATION:
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STRANDEDNESS: SI
             APPLICATION NUMBER:
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5. 5587311
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                                                                                                                                                                                                                                                                                                                         3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COBON, Stewart Gary MOORE, Joanna Terry
                                                                                                                                                                                                                                                                                                                                                                                   RIDING, George Alfred
RAND, Keith No. 5587311man
VENTION: DNA Encoding A Cell Membra
VENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WILLADSEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRISKANTHA, Alagacone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHNSON, Law Anthony York
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                                              07-AUG-1992
06-JUL-1988
                                                                                             JMBER: US 08/062,109
17-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David Harold
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                                                             US 07/926,368
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               07/242,196
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Pred. No.
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PRIOR APPLICATION DATA:

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US-08-461-004A-59
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--- rocal Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                  APPLICANT: KEMP, David Harold
APPLICANT: SRISKANTHA, Alagacone
APPLICANT: RIDING, George Alfred
APPLICANT: RAND, Keith No. 6235283man
TITLE OF INVENTION: DNA Encoding A Cell Membrane
TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTAGN NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
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                                                                                                                             COUNTRY:
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                    Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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RESULT 8
US-08-767-096-3
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                                                                                                                                                                        Sequence 3, Application US/08767096 Patent No. 5939284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                      GENERAL INFORMATION: APPLICANT: Cohen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                   APPLICANT: Cohen, Ph
APPLICANT: Young, Pe
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI2570
PTLING DATE: 19-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PI4912
FILING DATE: 16-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acid
                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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TELEFAX: 904136
                                                                                                                                                                                                                                                                               418
                                                                                                                                                                                                                                                                                                               108 MHVNL-----EIE-----
                                                                                                                                                                                                                                                                                                                                               362 RVLEAIRTSIGKEVFKVEILNCTQDIKARLIAEKL---LSKHVLRKLQACEHPIG-EWCM 417
                                                                                                                                                                                                                                                                                                                                                                                                                303 EFMDCGVY-MNRQSCYCPWKSRKPGPNVNINGCLLNEYYYTVSFTPNISFDSDHCKWYED 361
                                                                                                                                                                                                                                                                                                                                                                64 CLSKSKQTKLG-------CSK----VLVPEKLTQRIAQDVLR-LSSTE-PCGLRGCV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ELLDCGYHPESLLSDFDYWDYVPEPN-----LNEVIFEESTCQNL-----VKMLEN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: AU PH9196 FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 19-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 04-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                   ADDRESSEE:
                                                                                                                                                                                                                                                                               MYPKLLIKKNSATEIEEENLCDSLLKDQEAAYKGQNKCVKVDNLFWFQCADGYTTTYEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650 amino acids
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                                                                                                      Young, Peter R.
                                                                                                                     Cohen, Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                        Cohen,
 SmithKline
Swedeland
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17-MAY-1993
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                                                                                                                                      Patricia T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.48;
                                                                      R5
                                                                                     A Protein
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Beecham Corporation Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; I
Pred. No. 2
                                                                                   Phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 650;
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                                                                                     Binding Protein,
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; SEQ ID NO 3; LENGTH: 284; TYPE: PRT; ORGANISM: HOMO SAPIENS US-09-480-203-3
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; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-767-096-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-480-203-3
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Best Local S
Matches 35
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                TITLE OF INVENTION: A PRÔTEIN PHOSPHATASE 1 BINDING PRCTEIN TITLE OF INVENTION: R5
FILE REFERENCE: ATG-50033-2
CURRENT APPLICATION NUMBER: US/09/480,203
CURRENT FILING DATE: 2000-01-10
EARLIER APPLICATION NUMBER: 09/300,327
EARLIER FILING DATE: 1999-04-27
EARLIER APPLICATION NUMBER: 09/767,096
EARLIER APPLICATION NUMBER: 08/767,096
EARLIER FILING DATE: 1996-12-05
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Patricia T.W. (APPLICANT: Phillip Cohen APPLICANT: Peter R. Young
                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 --- IRMTFD------TWKSFTDF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 DSSVVPTFELTLVFKQENCSWTSFRDF 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 KSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRIVC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 PASISELLD-----CGYHPESLLSDFDYWDYVVPEPNLNEVIFEESTCONLVKMLENCLS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 23.8 nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Schreck, Patricia A. REGISTRATION NUMBER: 33,77
REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 19406-2799
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STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFNITELLDNIVSLTTAESESFYLDF-----PQPSADYLDFRNRLQTNHV-CLENCVL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                        Patricia T.W. Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 amino acids
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 7.2%;
23.8%;
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Pred. No. 1.3;
 Score
Pred.
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 72.5; DI
No. 1.3;
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                 DB
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                   4;
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                   Length 284;
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                                                              Query Match
Best Local Similarity
Matches 49 Conserv
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                                                                                                                                                                                                                                                             TELEFAX: (970) 668-2052 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                                                                                                                                        FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UB
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Apoptosis Modulators That Interact with the TITLE OF INVENTION: Huntington's Disease Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                         401 PEDISELL----HSITLLAHLT-GDTVIQGSATSLRAPPEPADSLTEACRQYGRETLAYL 455
                                                12 PASISELLDCGYHPESLLSDFDYWDYVV····--PEP--NLNEV-----
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 48
                                                                                                                                                                    ORGANISM: mouse
                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             NAME: Larson, Marina T
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENITELLDNIVSLTTAESESFVLDF------PQPSADYLDFRNRLQTNHV-CLENCVL 139
 --IFEESTCQNL-VKMLENCLSK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: USA
80443-5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Oppedahl & Larson PO Box 5270
                                                                                                                                                                                                                                                     756
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                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalchman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hackam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chopra, Vikramjit Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                       (970)
                                                                                         7.2%;
                                                                                                                                                                                                                                                                                                       668-2050
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                                                                                                                                            Huntington-interacting protein
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                                                                                                                                                                                                                                                                                                                                              32038
                                                                                                                                                                                                                                                                              9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.50 inch, 1.44 Kb storage
                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                 UBC.P-013US2
                                                                                          Score 72; DB Pred. No. 6.4;
                                                                            Mismatches
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                                                                                                     DB 4; Length 756
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-SKQTKLG-----CSKVLVPEK 83
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US-08-775-009-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 871 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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 224
                                   103 LRGCV---MHVNLEIENVCKKLDRIVCDSSV 130
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                                                                                                   58 VKML-ENCLSKSKQTKLGCSKVLVPE------
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/775,009 FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 5935783ris, LLP STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                             10 KNPASISEL----LDCGYHPESLLSDFDYWDYVV-----PEPNLNEVIFEESTCQ-NL
                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                        EEPATHNALAKIYIDSNNSPECFLRENAYYDSSVVGRYCEKRDPHLACVAYERGQCDLEL
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ISVTVKAFMTADLPNE-LIELLEKIVLDNSV 253
                                                                      IKVCNENSLFKSEARYLVCRK--DPELWAHVLEETNPSRRQLIDQVVQTALS-ETRDPEE
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Similarity 27.2%;
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                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                 Score 72; DB 2; Pred. No. 7.9;
                                                                                                       ---KLTORIAODVLRLSSTEPCG 102
                                                                                                                                                                                                                                                  Length 871;
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SOFTWARE: Patentin Ver
SEQ ID NO 2
LENGTH: 530
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CURRENT FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: PCT/CA97/00328
EARLIER FILING DATE: 1997-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BEAULIEU, MARTÍN
APPLICANT: LEVESQUE, ETÍC
TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE
TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1996-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR
                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 057
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                      APPLICATION NUMBER: US/08/890,865A FILING DATE: 10-JUL-1997 CLASSIFICATION: 435
                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1185 A
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1185 Avenue of the Americas
                  (212)391-0526
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28.6%; Pred. No. 5.7;
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                                                                              0575/54249
                                                                                                                                                                                                                                        Version
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                                                                                                                                                                                                  APPLICATION NUMBER: US/08/325,071
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,109
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F
FILING DATE: 27-NOV-1987
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CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA Encoding A Cell Membrane TITLE OF INVENTION: Glycoprotein Of A Tick Gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 NNGIVSRQIKPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPEF 215
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                                                                                                                   APPLICATION NUMBER: 07/242,196 FILING DATE: 06-JUL-1988
                                                                                                                                                                     APPLICATION NUMBER: US 07-FILING DATE: 07-AUG-1992
                 APPLICATION NUMBER: FILING DATE: 16-OC
                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 DYVVPEPNLNEVIFEESTCQNLV-----KMLENCLSKSKQTKLGCSKVLVPEKLTQ 86
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l Similarity 20.6%;
35; Conservative
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IBM PC compatible
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                                                                                                                                                                                                                                                                    UMBER: US/08/325,071
14-OCT-1993
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                                                                                                                                                                                                                                                                                                                          Release #1.0, Version #1.25
                                  AU PI4912
                                                                                  PCT/AU87/00401
                                                                                                                                                                                     US 07/926,368
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Pred. No. 12;
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US-08-461-004A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 70;
Best Local Similarity 22.6%; Pred. No.
Matches 40; Conservative 28; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                  FILING DATE: 04-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: AU P
FILING DATE: 27-NOV-1986
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Encoding A Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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APPLICATION NUMBER: US 0 FILING DATE: 17-MAY-1993
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COUNTRY:
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MOORE, Joanna Terry
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RIDING, George Alfred
RAND, Keith No. 6235283man
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                                                                       US 08/325,071
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Mismatches
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Search completed: October 11, 2002, 14:15:33 Job time: 34 secs
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TELEFAX: 202 672 5399
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-461-004A-56
                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 70; DB 4; Length 650; Best Local Similarity 22.6%; Pred. No. 8.9; Matches 40; Conservative 28; Mismatches 51; Indels
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APPLICATION NUMBER: AU P12570

FILING DATE: 19-JUN-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PH9196

FILING DATE: 27-NOV-1986

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 60042/152

TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/926,368
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/242,196
FILING DATE: 06-UUL-1988
PRIOR APPLICATION DATA: PCT/AU87/00401
APPLICATION NUMBER: PCT/AU87/00401
FILING DATE: 27-NOV-1987
PRIOR APPLICATION DATA: AU P14912
APPLICATION NUMBER: AU P14912
FILING DATE: 16-CCT-1987
PRIOR APPLICATION DATA: AU P14912
FILING DATE: 16-CCT-1987
                                                        421 KLLIKKNSATEIBEENLCDSLLKDQEAAXKGQNKCVKVDNLFWFQCADGYTTTYEMT 477
                                                                                                                                                                         303 EFMDCGVY-MNRQSCYCPWKSRKPGPNVNINECLLNEYYYTVSFTPNISFDSDHCKWYED 361
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                                                                                                                                                                                                                                                                                                                                                            51; Indels 58; Gaps
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Result No.

Database

71.5 7.1 510 1 GARD BACSU 71.5 7.1 566 1 T\$31_MOUSE 71.5 7.1 1818 1 Z294_HUMAN 71 7.1 1818 1 Z294_HUMAN 71 7.1 469 1 VLZ_BPV1 71 7.1 469 1 VLZ_BPV1 71 7.1 1005 1 E41Z_HUMAN 70.5 7.0 333 1 DCAM_RAT 70.5 7.0 334 1 DCAM_MOUSE 70.5 7.0 334 1 DCM2_MOUSE 70.5 7.0 334 1 DCM2_MOUSE 70.5 7.0 334 1 DCM2_MUSSP 70.5 7.0 334 1 DCM2_MUSSP 70.5 7.0 334 1 DCM2_HUMAN	7.1 560 7.1 1818 7.1 1818 7.1 459 7.1 469 7.1 814 7.1 814 7.1 1005 7.1 333 7.0 334 7.0 334 7.0 334 7.0 334 7.0 530
510 516 1818 1818 179 169 169 105 105 133 133 133 133 133 133 133 13	510 1 GARD_BACSU P42240 5566 1 TS13_MOUSE 001755 1818 1 Z294_HUMAN 94872 1791 RL5_BUCAK P46178 469 1 VL2_BPV 1 P03109 814 1 SYV_RICPR 092cn6 1005 1 E412_HUMAN 943941 333 1 DCAM_RAT 917708 333 1 DCAM_MOUSE P31154 334 1 DCM2_MOUSE P82185 530 1 UDBH_HUMAN 075795
	1 GARD_BACSU P42240 1 TS13_MOUSE 001755 1 Z294_HUMAN 094822 1 RL5_BUCAK P46178 1 VL2_BPV1 P03109 1 SYV_RICPR 093010 1 SYV_RAT 0920n6 1 E412_HUMAN 043991 1 DCAM_RAT P17708 1 DCM1_MOUSE P31154 1 DCM2_MOUSE P32185 1 UDBH_HUMAN 075795
1 GARD_BACSU 1 TS13 MOUSE 1 TS13 MOUSE 1 Z294_HUMAN 1 RL5_BUCAK 1 VL2_BPV1 1 SYV_RICPR 1 E4L2_HUMAN 1 DCAM_RAT 1 DCAM_RAT 1 DCM2_MOUSE 1 DCM2_MUSSP 1 UDBH_HUMAN	P42240 001755 094822 P46178 P03109 092cn6 043491708 P17708 P31154 P82185 075795
GARD_BACSU TS13_MOUSE TS13_MOUSE 2294_HUMAN RL5_BEVCAK VI.2_BPV1 SYV_RICPR E41.2_HUMAN DCAM_RAT DCM1_MOUSE DCM2_MOUSE DCM2_MUSSP UDBH_HUMAN	P42240 001755 094822 P46178 P03109 092cn6 043491708 P17708 P31154 P82185 075795
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ALIGNMENTS

Title: Perfect score: Sequence:

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Scoring table:

Searched:

Db	VΩ	Db	Qy	дd	Ωу			SQ	S E E	DR	DR	3 6	38	33	33	3 8	38	S	8 3	5 5	3 2	RA	RP	20 22	P.F.A	RP	RN	<u> </u>	200	200	GN	DE	DJ ;] [AC AC	ID
719 IINMKEGLLEFADRKFIKLGKVDGGGWQTLTL 750	124 IVCDSSVVPTFELTLVFKQENCSWTSFRD-FFFSRGFFSSGFRTTLIL 170	661 QPDALLKTAEIILVTDTQTIVFDVISTVHPCGLNIIKKFYQYLKINIPIDVLPNKIEW 718	84 LTQRIAQDVLRLSSTEPCGLRGCVMHVNLE	613 NPDVELSDYVMWEYNVPENTIVFSLHVNTLSRYKLLKMKSKNHNASEK 660	24 HPESLLSDFDYW	Matches 42; Conservative 23; Mismatches 52; Indels 51; Gaps 8;	Match 9.0%; Score 90.5	SEQUENCE 1056 AA; 121649 MW; 2368616B67AEAD31 CRC64;		TRANSFAC; T035		FMpt . D/3905: D/307966 1.	or send an email to license@isb-sib.ch).	entities requires a license agreement (See http://www.isb-sib.ch	modified and this statement is not removed. Usage by and for commercial	the purphed and inclinations as long as its content is in no	between the Swiss Institute of Bioinformatics and the EMBL outstatic	This SWISS-PROT entry is copyright. It is produced through a		GENES AND	-i- FINCTION: INVOLVED IN THE TRANSCRIPTION OF BOTH RIBOSOMAL.			oubmitted (DEC-1994) to the EMBL/Vehbank/DDBO databases.	Mizuta K.;	SEQUEN		NCBI_TaxID=4932;	Saccharomycetales: Saccharomyc	Saccharomyces cerevisiae (Baker's yeast).		RIC1 protein.	16-OCT-2001 (Rel. 40, Last	Ol-FEB-1945 (Rel. 31, Created)	P40395;	1

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Addmantides P. G., Scherer S.E., Helt R.A., Evans C.A., Gocayne J.D.,
RA Addmantides P. G., Scherer S.E., Hilb, W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Fannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Pengelista C.C., Ferraz C., Ferritera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Genbar S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hostin D., Houston K.A., Nusand T.J., Lin, T., Houck J.,
RA Mount S.M., Wattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Wallson D.R., Nelson D.L.,
RA Mount S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spien H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Milliams S.M., Woodag T., Wollan M., Zhu S., Zhu X., Smith T.,
RA Glibs R.A., Myers E.W., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Glibs R.A., Myers E.W., Dann S., Dong W., Zhou X., Zhu X., Zhu X., Smith H.O.,

"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000)
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01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ran-binding protein 16.
RANBP16 OR CG9126.
RANBP16 OR CG9126.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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01-MAR-2002 (Re
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                                                                                                             complex (By similarity).
SIMILARITY: BELONGS TO THE EXPORTIN FAMILY.
                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic,
                                                                                                                                                                                                              similarity)
                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBB7700; OBB198;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
Bloom's syndrome protein homolog (EC 3.6.1.
                                                                                                                                                                                                                                                                                                       level.";
Biochim. Biophys. Acta 1398:377-381(1998).

-!- FUNCTION: PARTICIPATES IN DNA REPLICATION AND MAY PARTICIPATE IN REPAIR. EXHIBITS A MAGNESIUM-DEPENDENT ATP-DEPENDENT DNA-HELICASE REPAIR. EXHIBITS A MAGNESIUM-DEPENDENT ATP-DEPENDENT DNA IN A 3'-5'
                                                                                                                                                                                                                                                                                                                                                                                       Seki T., Wang W.-S., Okumura N., Seki M., Katada T., Enomoto "cDNA cloning of mouse BLM gene, the homologue to human Bloom syndrome gene, which is highly expressed in the testis at the
          EMBL; Z98263; CAB10933.1;
EMBL; AB008674; BAA32001.1
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/C; TISSUE=Testis, Spe
MEDLINE=98322127; PubMed=9655940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Point mutations causing Bloom's syndrome helicase activities of the BLM protein."; Oncogene 17:2565-2571(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., FUNCTION, AND MEDLINE=99054654; PubMed=9840919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLM_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0030709; Ranbp16. Nuclear protein; Transport; Pi
                                                            or send
                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bahr A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                      DIRECTION: Nuclear (By similarity).
SUECELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS 12-14 DAYS AFTER
BIRTH (CORRESPONDING TO THE PACHYTENE PHASE) AND AT MUCH LOWER
BIRTH (CORRESPONDING TO THE PACHYTENE PHASE) AND AT MUCH LOWER
BIRTH (CORRESPONDING TO THE PACHYTENE PHASE) AND AT MUCH LOWER
BIRTH (CORRESPONDING TO THE PACHYTENE PHASE) AND AT MUCH LOWER.
                                                                                                                                                                                          LEVELS IN BRAIN, HEART, KIVER, LUNG, THYMUS, KIDNEY AND SPL
SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
SIMILARITY: CONTAINS 1 HDRC DOMAIN.
                                                                                                                                                                                                                                                                                             DIRECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NYLATVPNLQHEV-----VQALVSLL-----AKLTKYGWEDSYKEEMVFQNLLEDVKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYVVPEPNLNEVIFEESTCONLVKMLENCLSKSKOTKLGCSKVLVPEKLTORIAODVLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LQGSVEHCTIGVQ----ILSQLVCEMNSVVEMDVQVSFSKMRKIATSFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTEPCGLRGCVMHVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRD
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AE003500; AAF48542.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                          an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Transport;
E 1098 AA; 125532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                      gene,
                                                                                                             non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Graeve F., Kedinger C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
               BAA32001.1;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND TISSUE
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25.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Ver
Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIFICITY.
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                                                                                               Usage by
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                                                                                                                               restrictions
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                                                                                                                                                                                                                                         4 DAYS AFTER
MUCH LOWER
                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                        Bloom's
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                                                                                                                                                 a collaboration -
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                                                                                                                                                outstation
                                                                                                              in
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
NP_BIND
SITE
                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Voltage-dependent calcium channel gamma-3 subugated calcium channel gamma-3 subunit).
                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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Pfam; PF00271; helicase_C;
Pfam; PF00570; HRDC; 1.
TISSUE-Cerebellum; MEDLINE-99236653;
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                      CCG3_HUMAN
060359;
                 SEQUENCE FROM N.A.
                                  NCBI_TaxID=9606;
                                                            Homo
                                                                    CACNG3
                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                             SEQUENCE
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InterPro;
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                                                                                                                                                                                                                                                       SDFDYWDYVVPEPNLNEVIFEEST----CQNLVKMLENCLSKSKQTKI.GCSKVLV--PEKL
                                                          sapiens (Human).
                                                                                                                                                                                       FKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGF 174
                                                                                                                                                                                                       TTHKSD----AGTSKDCDAQQIRIQQQLIHV---MEHICKLVD---
                                                                                                                                                                                                                       TQRIAQDVLRLSSTEPCG-----LRGCVMHVNLEIENVCKKLDRIVCDSSVVPTFELTLV 139
                                                                                                                                                                                                                                        NDYDI-DFVPPSP--EEIISTASSSLKCSSMLKDLDD--SDKEKGILSTSEELLSKPEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00490; HELICC;
SM00341; HRDC; 1.
                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00690; DEAH_ATP_HELICASE;
                                                                                                                                                                      NCGTELLQ-----
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IPR002464;
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229
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                                                                                                                              STANDARD;
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 PubMed=10221464
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                                          Chordata;
Primates;
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DEAH_ATP_helicase.
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                                                                                                                                                                      -QRNIRRKLLAEAGF
                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                         E -> EE (IN REF. 2).
V -> M (IN REF. 2).
WN -> RT (IN REF. 2).
MISSING (IN REF. 2).
T -> A (IN REF. 2).
T -> N (IN REF. 2).
V -> L (IN REF. 2).
V -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                   Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       K->A: REDUC
ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITIES
                                                                                                                                                                                                                                                                                                                                                                                               C->S:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION Q->P: REDUCED ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVITIES
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ATP (BY SIMILARITY).
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                                         Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ASP
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                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                               v
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18;
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                                                                                   subunit
                                           Hominidae;
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                                                                                                                                                                                                                                                                                           Length 1416;
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                                                                                  (Neuronal
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                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                               HELICASE
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                                                                                  voltage-
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RESULT 5
CED4_CAEEL
ID CED4_CAEEL
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Best Local S
Matches 41
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TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XIA J.-H., Zhang H.-L., Tang X.-X., YU K.-P., Pan Q., Dal H.-P.;
"Cloning of human calcium channel gamma-3 subunit.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: THOUGHT TO STABILIZE THE CALCIUM CHANNEL IN AN
INACTIVATED (CLOSED) STATE.
-I- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FIVE SUBU
ALPHA-1, ALPHA-2/DELTA, BETA AND GAMMA.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- DISCASE: CANDIDATE GENE FOR A FAMILIAL INFANTILE CONVULSIVE
DISCASE: CANDIDATE MORE OF A FAMILIAL INFANTILE CONVULSIVE
DISCASE: CANDIDATE MORE OF A FAMILIAL INFANTILE CONVULSIVE
DISCASE: CANDIDATE MORE OF A FAMILIAL INFANTILE CONVULSIVE
DISCASE: CANDIDATE BELONGS TO THE PMP-22 / EMP / MP20 FAMILY. CACING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99425270; PubMed=10493829;
Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S.,
Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence
human chromosome 16p and 16q.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium channel gamma-2 and gamma-3 subunits: neurologic implications.";
Mayo Clin. Proc. 74:357-361/1000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF100346; AAD22739.1; -. EMBL; AC004125; AAC15246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Bioinformati
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                                                                                                                                                                       ELTLYFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRLYKKKLYSLIGTTV
                                                                                                                                                                                                                                                                     LRLSST-EPCGLRGCVMHVNLEIENVCKKLD--
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PF00822; PMP22_Claudin; 1.
Channel; Transmembrane. Ton the
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                                                                                                                                                                                                                      MTHSGLWRTCCLEGA-----FRGVCKKIDHFPEDADYEQDTAEYLLRAVRASSVFPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF134640; AAF42975.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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315
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Zhang H.-L.,
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135
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124 P
155 P
201 P
35548 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79;
Pred. No.
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POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                            RHNVILSAGIFFVSAGLSNIIGIIV
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                                                                                                                            155
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P30429;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cell death protein 4.
CED-4 OR C35D10.9.
                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                  Pfam; PF00619; CARD; 1.
Pfam; PF00931; NB-ARC; 1.
SMART; SM00114; CARD; 1.
PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; X69016; CAA48781.1; -. EMBL; U21324; AAA62564.1; -. WormPep; C35D10.9; CE01203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Caenorhabditis elegans cell death gene ced-4 encodes a novel protein and is expressed during the period of extensive programmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93161939; PubMed=1286611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fulton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Development 116:309-320(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuan
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                             InterPro;
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 180
                      185
                                             146
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                                                                                           116
                                                                                                                  65
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                                                                                                                                                         KNPASISELLD-CGYHPESLLSDF--DYWDYVVPEPNLNE--VIFEESTCQNLVKMLENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J., Horvitz H.R.;
 G
                - IG
                                                                  VCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRLVKKKLYSL
                                                                                           ---DRKLLLG----NVPKQMT---
                                                                                                                                         RQASELGPLIDFFNYNNQSHLADFLEDYIDFAINEPDLLRPVVIAPQFSRQML-----
                                                                                                                LSKSKOTKLGCSKVLVPEKLTORIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRI
                                                                                                                                                                                         45;
 181
                       186
                                                                                                                                                                                                   Similarity
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IPR002182; NB-ARC
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                                                                                                                                                                                        Conservative
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62878 MW;
                                                                                                                                                                                                   7.98;
24.78;
                                             EMCDLDSF -- FLFLHGRAGSG -- KSVIASQAL -- -- SKSDQL
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                                                                                                                                                                                      23;
                                                                                                                                                                                                   Score 79;
Pred. No.
                                                                                                                                                                                                                                                ATP
                                                                                                                                                                                                                                                             CARD.
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DB2A7969BDA50AF8 CRC64;
                                                                                                                                                                                        Mismatches
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                                                                                           -CYIR-----EYHVDRVIKKLD--
                                                                                                                                                                                        46;
                                                                                                                                                                                                              Length 549
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RESULT 6
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01-MAR-2002
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                            Complete proteome. BINDING 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
-:- CATALYTIC ACTIVITY: ADP-glucose + {(1,4)-alpha-D-glucosyl}(N1) =
-:- ADP + {(1,4)-alpha-D-glucosyl}(N+1).
-:- PATHWAY: Glycogen biosynthesis; second step.
-:- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube: Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGA_AQUAE 066935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aquifex aeolicus.
Bacteria; Aquificales;
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                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Glycogen biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001296; Glycos_transf_1.
Pfam; PF00534; Glycos_transf_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000704; AAC06894.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392:353-358(1998).
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353 YASSDFILM
                                                               302
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                              ILSSGFRLV 177
                                                                                              HVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSSGFRRTL
                                                                                                                                                                                              IVFSDLITTVSPTYAKEIQTQEYGYGLEGVLKKYSYKLRGILNGIDYEVWNPEKDKYIYQ
                                                               ----ILNCAEEMSKLNANFVFLGTGEYENAFLDVSKIYKNFKVF----AEFNEGFARKL
                                                                                                                              NYSLRNYSKKFKNKEFLSKELGIEAEKPLISFINRFTHQKGVEL
                                                                                                                                                             ESTCQNLVKMLENCLSKSKQTKLGCSKVLVP--EKLTQRIAQDVLRLSSTEPCGLRGCVM 108
                                                                                                                                                                                                                                                               1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
nthase (EC 2.4.1.21) (Starch | ba
                                                                                                                                                                                                                                                               Conservative
361
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                                                                                                                                                                                                                                                                                                                              15 /
53457 MW;
                                                                                                                                                                                                                                                                              19.6%;
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                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                              Score 78.5; DI
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                              ADP-GLUCOSE (BY SIMILARITY). B896172D0D3DB27D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tation update)
(Starch [bacterial glycogen]
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ID LON2_M
AC P93648
DT 15-DEC
DT 15-DEC

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P93648; 15-DEC-1998 15-DEC-1998

(Rel. 37, Created) (Rel. 37, Last seq.

sequence

RESULT

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RESULT 8
Y42B_RHISN
ID Y42B_R
AC P55729
DT 01-NOV
DT 01-NOV
DT 16-CT
DE Putati
GN Y42B.
OS Rhizob
OG Plasmi
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Matches 34
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P55729;
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00004; AAA; 1.
Pfam; PF02190; LON; 1.
PRINTS; PR00830; ENDOLAPTASE.
SMART; SM00382; AAA; 1.
SMART; SM00464; LON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rapp W.D., Barakat S.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS
                                     01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
Putative transposase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593; AAA.
InterPro; IPR003959; AAA_subfam.
InterPro; IPR003111; LON.
 Rhizobium sp.
Plasmid sym p
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion; Transit peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U85495; AAC50021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. B73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Panicoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LON2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                    636
                                                                                                                                                                                            118
                                                                                                                                                                                                                    579
                                                                                                                                                                                                                                                                    528
                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                            5 GSLSSKNPAS-ISELLDCGYHPESLLSDFDYWDYVVPEPNLNEVIFEESTC-QNLVKMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY OF ATP-DEPENDENT PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease
                                                                                                                                                                    CRE
                                                                                                                                                                                           CKK
                                                                                                                                                                                                                                         NCLSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVN-----LEIENV 117
                                                                                                                                                                                                                                                                    GKGHSGDPASALLELLD----PEQNVNFLDH--YLDVPIDLSKVLF---VCTANVIEMIP
                                                                                                                                                                                                                   NPL-LDRMEIIAIAGYITDEKM--HIARDYLEKNTRQACGIKPEQYEVTDTALLALIENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S16.002
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                    638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001984; Lon_endopep.
                                                                                                                                                                                                                                                                                                                                                                    455
863
964 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease;
  pNGR234a.
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homolog
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LON_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40,
                                                                                                                                                                                                                                                                                                                                                                                           964
462
                                                                                                                                                                                                                                                                                                                             7.8%;
                                                                                                                                                                                                                                                                                                                                                                      105659 MW;
                                       Y4ZB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
2, mitochondrial precursor
                                                              Created)
Last sequence
              NGR234)
                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Multigene family;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                  ВY
                                                                                                                                                                                                                                                                                                                                                                                         MITOCHONDRION (POTENTIAL).
LON PROTEASE HOMOLOG 2.
ATP (POTENTIAL).
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
D78A6C6B0F8A6D9E CRC64;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                78.5;
No. 15;
                                                               update)
                                                                                                    356
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                                                                                                    A
                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                            Length 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae; PACC clade;
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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    578
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLM_HUMAN P54132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Bloom's syndrome protein (EC 3.6.1.-) (RecQ protein-like 3) (DNA helicase, RecQ-like, type 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                      Karow J.K., Chakraverty R.K., Hickson "The Bloom's syndrome gene product is J. Biol. Chem. 272:30611-30614(1997).
                                                                                                                                                                                                                                                                                                                                             Ellis N.A., Groden J., Ye T.-Z., Proytcheva M., German J.;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS BS
MEDLINE-96069866; PubMed-7585968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLM OR RECQL3 OR RECQ2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
Hypothetical protein; Transposable element;
DNA-binding; DNA recombination; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000108; AAB91960.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular basis of symbiosis between Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                              NUCLEAR LOCALIZATION SIGNAL. MEDLINE-98049834; Pubmed-9388480;
                                                                                                                                                                                                    MEDLINE-98049515; PubMed-9388193;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perret X
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                            Kaneko H.,
                                                                                                                                                                                                                              rissue-B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                 Bloom's syndrome gene product 83:655-666(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNDAQIGRTIAIESGATYIFDKGYCHYGWWTAIAEAKAFFVTRPKSNMGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCDSSVVPTFEL---TLVFKQENCS---WTSFRD---FFFSRGRFSSGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLTQRIAQDVLRLSSTEP-----CG-----LRGCVMHVNLEIENVCKKL----DRI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRQTRREGRAMLRLIDSTPIPLGKLCGWAKSNGRIRGMKMHVVYDPDSDCPRLLDITDAN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                            Orii K.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
     Furuichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39775 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%;
25.2%;
Matsui E., Shi
i Y., Hayakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77.5;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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                            Shimozawa
                                                                                                                                                                                                                                                                                                                                                                          Straughen J., Lennon D.J., Ciocci S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α.,
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s:
                                                                                                                                                                                                                                                                                                                                                                                                                           ARG-672; ILE-843 AND SER-1055
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                                                                                                                                                .D.;
3′-5′
  Kasahara
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                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                           RecQ helicases.";
                            Ŧ.,
     Kondo
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                         Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
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Shimamoto

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     Best Local Similarity
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Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00570; HRDC; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem.
[4]
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SITE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U39817; AAA87850.1; MIM; 604610; -.
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                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLM (the causative gene of Bloom syndrome) protein translocation into the nucleus by a nuclear localization signal.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOSOMAL INSTABILITY.

SIMILARITY: BELONGS TO THE HELICASE FAMILY.

SIMILARITY: BELONGS TO THE DOMAIN.

SIMILARITY: CONTAINS 1 HDRC DOMAIN.

DATABASE: NAME-BILMbase; NOTE-BLM mutation db

WHW-"http://www.uta.fi/imt/bioinfo/BLMbase/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR, SUBCELLULAR LOCATION: NUCLEAR, DISEASE: DEFECTS IN BLM ARE THE CAUSE OF BLOOM SYNDROME (BS), A AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY PROPORTIONATE PRE AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY PROPORTIONAL RECESSIVE PROPORTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PARTICIPATES IN DNA REPLICATION AND MAY PARTICIPATE IN REPAIR. EXHIBITS A MAGNESIUM-DEPENDENT ATP-DEPENDENT DNA-HELICASE ACTIVITY THAT UNWINDS SINGLE- AND DOUBLE-STRANDED DNA IN A 3'-5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIRECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00490; HELICC;
SM00341; HRDC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00690; DEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001410; DEAD.
IPR002464; DEAH_ATP_helicase.
IPR002121; HRDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND HYPERPIGMENTED SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Vaury
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                                                                                       1417
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y C., Barakat A.,
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     7.7%;
31.8%;
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                                                                                                                                 -> F (IN BS).
/FTId=VAR_009140.
C -> S (IN BC)
                                                                                       Ψ×
                                                                                                                                                                                                                                             -> E (IN BS).
/FTId=VAR_009138.
C -> Y (IN BC)
                                                                                                                                                                                             /FTId=VAR_009139.
C -> F (TN BC)
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION Q -> R (IN BS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP
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                                                                                                                                                                                                                                                                                                                                  T -> I (IN BS).
/FTId=VAR_006902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ASP
                                                                                    /FTId=VAR_006903;
W; 423DF5F381194E11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_006901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-ASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREDISPOSITION TO MALIGNANCY;
        No
                               77;
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DB
34;
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                            Length 1417;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL (POTENTIAL)
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                                                                                                                                     Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
PRODOM; PD003376; DIL; 1.
PRODOM; PD003376; DIL; 1.
SMART; SM00015; IQ; 6.
SMART; SM000242; MYSS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MY5A_RAT STANDING
Q90YF3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up)
16-OCT-2001 (Rel. 40, Last annotation
16-OCT-2001 (Rel. 40, Last annotation)
                                                                                                        Myosin;
Coiled c
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_RAT
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DOMAIN
                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Futaki S., Murata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                              PROSITE;
                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                    InterPro; IPR002710; InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                   FORMATION (BY SIMILARITY).
SUBUNIT: MAY BE A HOMODIMER, WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                         BE REQUIRED FOR SOME POLARIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM---QELNPETSTDCDARQISLQQQLIHV---MEHICKLIDTIPDD
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                                                                                                                                                                                                               PF01843; DIL;
                                                                                                                                                                                                                                                         P08799;
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                                                                                                                                                                                                      PF00612; IQ; 6
                                                                                                         coil;
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                                                                                                                    Repeat; ATP-binding;
                                                                                                                              PS50096;
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IPR001609;
 766
789
814
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862
885
914
1314
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1418
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MYOSIN
IQ 1.
IQ 2.
IQ 3.
IQ 4.
IQ 5.
IQ 6.
COILED
COILED
DILUTE.
                                                                                                                   Calmodulin-binding; Actin-binding;
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Sciurognathi;
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           COIL
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heavy chain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          PROCESS INVOLVED IN DENDRITE
                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATES WITH MULTIPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ
           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muridae;
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Best Local S
Matches 42
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01-JUN-1994 (Rel. 2
16-OCT-2001 (Rel. 4
Myosin Va (Myosin 5
heavy chain P190)
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DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                  Espreafico E.M., Cheney R.E., Matteoli M., Nascimento A.A., de Camilli P.V., Larson R.E., Mooseker M.S.; "Primary structure and cellular localization of chicken brain myosin-V (p190), an unconventional myosin with calmodulin light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHICK
               + + +
                                                                                                                                                                 - J
                                                                                                                                                                                                                                                                                                                   FEBS
                                                                                                                                                                                                                                                                                                                           Sanders G., Lichte B., Meyer H.E., Kilimann M.W.;
"CDNA encoding the chicken ortholog of the mouse dilut
Sequence comparison reveals a myosin I subfamily with
terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1720
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                                                                                              -
                                                                                                                                                                                           chains.";
                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=93107155;
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 1154-1163
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-93012002; PubMed-1383040;
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q02440;
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                                                                Cell Biol. 119:1541-1557(1992).

FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGESTEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILMAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRE FORMATION (BY SIMILARITY).

SUBCRIPTION OR MYOSIN LIGHT CHAINS.

SUBCRIPTION OR MYOSIN LIGHT CHAINS.
TISSUE SPEĆIFICITY: NEURONAL AND NONNEURONAL CELLS SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DC SIMILARITY: CONTAINS 6 10 DOMAINS.
SIMILARITY: CONTAINS 1 DILUTE DOMAIN.
                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                   Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILSSGFRLVKKK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVVKQMFYIVGAITLNNLLLRKDMCSWSKGMQIRYNVSQLEEWLRDKNLMNSGAKETLEP 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HETIQGV---SGVKPTGLRKRTSSIADEGTYTLDSILRQLNSFHSVMCQHGMDP--ELIK 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRIAQDVLRLSSTEPCGLRGCVMHVNLE----IENVCKKLD---RIVCDSSVVPTFEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHCLTNFDLAEYRQVLSDLAIQIY - - - - - QQLVRVLENIL - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIQAAQLLQVKKK 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TSFRDFFFSFGRFSSGFRRT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                311:295-298(1992).
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643
1733
1828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40,
5A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29,
                                                                                                                                                                                                                                                            PubMed=1469047;
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665
1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Myosin-V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%;
21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
(Dilute myosin heavy chain, non-muscle) (Myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
ACTIN-BINDING (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĄĄ
                                                                                                                                   HAT CAN MOVE IN LARGE EAT OF THE ACTIN FILAMENT OR ALTERNATIVELY, IT MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                        dilute gene product. with conserved C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QPMIVSGMLE
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                           DOMAIN
                                      OF THE BRAIN
                                                                                                                      IN DENDRITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
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MY5A_MOUSE STAN Q99104; Q99104 (Rel. 2 01-JUN-1994 (Rel. 2 10-OCT-2001 (Rel. 4 MYOSIN VA (MYOSIN 5 MYOSA OR DILUTE.

29, 40, 5A)

Created)
Last sequence update)
Last annotation update)
(Dilute myosin heavy chain, non-muscle).

STANDARD;

PRT;

1853

(Mouse)

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RESULT 12
MY5A_MOUSE
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam: PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PrODom; PD000355; myosin_head; 1.
ProDom; PD003376; DIL; 1.
SMART; SM00015; IQ; 6.
SMART; SM00242; MYSC; 1.
PROSITE: PS50096; IQ; 6.
                                                                                                                                                                                                                                                  MOD_RES
CONFLICT
SEQUENCE
                                         1721
                                                                                                                                                                   1561
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                  1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X67251; CAA47673.1; -. EMBL; Z11718; CAA77782.1; -. HSSP; P08799; IMMG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                          1606
                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01843; DIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                              168
                                                                                                       137
                                                                                                                                              86
                                                                                                                                                                                       26
                                                             LILSSGFRLVKKK
                                                                                  QVVKQMFYIIGAVTLNNLLLRKDMCSWSKGMQIRYNVSQLEEWLRDKNLMNSGAKETLEP
                                                                                                                                                                  EHCLTNFDLAEYRQVLSDLAIQIY - - - - - QQLVRVLENIL - -
                                                                                                                                                                                       ESTTSDEDAMDAAAAANTEESTCONFAKWTENCTSKSKOLKTCCSKATAbektl
                                         LIQAAQLLQVKKK 1733
                                                                                                                         HETIQGV---SGVKPTGLRKRTSSIADEGTYTLDSIIRQLNSFHSVMCQHGMDP--ELIK
                                                                                                                                             QRIAQDVLRLSSTEPCGLRGCVMHVNLE----IENVCKKLD---RIVCDSSVVPTFEL--
                                                                                                                                                                                                                                                                                                                                                                                                            ; Repeat; ATP-binding;
coil; Phosphorylation
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000048; IQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002710; DIL.
                                                                                                                                                                                                                                                                        767
790
815
838
863
888
916
1315
1661
1661
1633
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                                                                                                                                                                                                                                                                       766
789
814
817
837
862
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915
915
1239
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1766
666
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                                                             180
                                                                                                      ---TLVFKQENCSW-----
                                                                                                                                                                                                                      21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin_head
                                                                                                                                                                                                                                                    212381 MW;
                                                                                                                                                                                                                             7.78;
                                                                                                                                                                                                        3
3;
                                                                                                                                                                                                                                                                                          IQ 1.
IQ 2.
IQ 3.
IQ 4.
IQ 5.
IQ 6.
COILED COIL (POTENTIA COILED COIL (POTENTIA DILUTE.
DILUTE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                     Score 77;
Pred. No.
                                                                                                                                                                                                                                                  PHOSPHORYLATION (POTENTIAL)
E -> EQ (IN REF. 2).
W; 0538B278DFC09F6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding; Actin-binding,
                                                                                                                                                                                                                                                                                 ACTIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                  MYOSIN HEAD-LIKE
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                      DB 1;
46;
                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                      TSFRDFFFSRGRFSSGFRRT---
                                                                                                                                                                                                           ;09
                                                                                                                                                                                                                                Length 1829;
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                                                                                                                                                                  --- OPMIVSGMLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ω
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                                                                                                                                                                                                          Gaps
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                                                                                 1720
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Best Local S
Matches 42
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DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000355; myosin_head; ProDom; PD003376; DIL; 1. smART; SM00015; IQ; 6. smART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01843; DIL; 1.
pfam; PF00612; IQ; 6.
pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Swiss Institute of Bioinformatics and the Electron to the Bioinformatics and the Bioinformat
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STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-91141583; PubMed-1996138;
Mercer J.A., Seperack P.K., Strob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 352:547-547(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jenkins N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercer J.A.,
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 349:709-712(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jenkins N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Novel myosin heavy chain
                                                         Local Similarity nes 42; Conser
                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 DILUTE DOMAIN. SIMILARITY: CONTAINS 6 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVOLVED IN DENDRITE FORMATION.
SUBUNIT: MAY BE A HOMODIMER, WHICH
CALMODULIN OR MYOSIN LIGHT CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MAY BE ALTERNATIVELY, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:105976; Myo5a.
rPro; IPR002710; DIL.
rPro; IPR000048; IQ.
rPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A46761; A46761.
; P08799; 1LVK.
ESLLSDFDYWDYVVPEPNLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X57377; CAA40651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                      coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                                                                                                     766
789
814
837
862
862
1314
                                                                                                                                                                                                                      1685
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seperack P.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding;
                                                                                                                                        AA;
                                                                                                                                                      788
813
836
861
861
913
1237
1443
1790
1790
170
665
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQ; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE INVOLVED IN MELANOSOME TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Rođentia;
                                                                            21.8%;
                                                                                                                                        215594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoded
                                                         33;
                                                                                                                                                  MYOSIN HEAD-LIKE.

10 1.

10 2.

10 3.

10 4.

10 5.

10 6.

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

DILUTE.

ATP (POTENTIAL).

ACTIN-BINDING (POTENTIAL).

PHOSPHORYLATION (POTENTIAL).

PHOSPHORYLATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strobel M.C.,
                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strobel M.C., Copeland
                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHICH
                                                                                                                                        503E93D48CA6B766 CRC64;
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                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine
                                                                                DB
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATES WITH MULTIPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSPORT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dilute
                                                         60;
                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLARIZATION PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Actin-binding;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                         58;
                                                       Gaps
                  85
                                                         9
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MYSAHUMAN
ID MYSAH
ID 16-OCT
DT 16-OCT
RP MYSSH
RP TISSUE
RA MEDLIN
RA JAbado
RT MUTATI
RA JABADO
RT MUTATI
RA JABADO
RT MUTATI
RA JABADO
RT TISSUE
RA ENGLE
RA ENGLE
RA ENGLE
RA ENGLE
RA MODOLE
RA MODLIN
RA EGGUEN
RA SUDMITT
RA SUDMIT
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                                                                                                                                                     Jenkins N.A.;
Jenkins N.A.;
"Cloning and regional assignment of the |
"Cloning and regional assignment of the |
"(MYH12) gene to chromosome band 15q21.";
(MYH12) Genet. 69:53-58(1995).
Edgar A.J., Bennett J.P.;
"Inhibition of dendrite formation in melanocytes transfected with antisense DNA to myosin V.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ dat [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSY4II: Q9UE30; Q9UE31; Q07902; Q16249; O60653; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin Va (Myosin 5A) (Dilute myosin heavy chain, (Myosin heavy chain 12) (Myoxin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT CYS-
MEDLINE=97351514; PubMed=9207796;
Pastural E., Barrat F.J., Dufourcq-Lagelouse R.,
Jabado N., Seger R., Griscelli C., Fischer A., d
"Griscelli disease maps to chromosome 15q21 and
mutations in the myosin-Va gene.";
Nat. Genet. 16:289-292(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1685
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                                                                                                                                                                                                                                                                                                                                                                 "Cloning, analysis, and chromosomal localization of myoxin (MYH12), the human homologue to the mouse dilute gene."; Genomics 19:407-416(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=94245227; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1745 LIQAAQLLQVKKK
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                                                                                                                          SEQUENCE
                                                                                                                                                Cytogenet.
                                                                                                                                                                                                                                                                     Moore K.J., Testa J.R.,
                                                                                                                                                                                                                                                                                           MEDLINE=95136715;
                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1061-1498 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Engle L.J., Kennett R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 638-1477 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jabado N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pastural E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERRATUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Barrat F.J., Dufourcq-Lagelouse R., (Seger R., Griscelli C., Fischer A., de . 23:373-373(1999).
                                                                                                                            1358-1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zimmermann R., Vosberg cDNA for human myosin
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                                                                                                                                                                                                                                                                   PubMed=7835087;
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TREASE REPORTED TO THE PROPERTY OF THE PROPERT
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Pfam; PF00063; myosin_head; 1.
Pfanr; PF00063; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1
ProDom; PD00355; myosin_head; 1
ProDom; PD003376; DIL; 1.
SMART; SM00015; IQ; 6.
SMART; SM00242; MYSc; 1.
PROSITE; PS50096; IQ; 6.
Myosin; Repeat; ATP-binding; Call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U90942; AAD00702.1; -. EMBL; V07759; CAA69035.1; -. EMBL; V07759; CAA69036.1; -. EMBL; Z22957; CAA690533.1; -. EMBL; S74799; AAB33211.1; -. EMBL; S74799; AAB33211.1; -. EMBL; S74799; AABC14188.1; -. HSSP; P08799; IMND. MIM; 160777; -. MIND.
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Nature 400.590-593(1999).

-:- FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE
-:- FUNCTION: PROCESSIVE ACTIN-BASED MOTOR THAT CAN MOVE IN LARGE
STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMENT.

MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY
BE REQUIRED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002710; DIL.
InterPro; IPR000048; IQ.
InterPro; IPR001609; myosin_head.
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GS IS A RARE AUTOSOMAL RECESSIVE DISORDER THAT RESULTS IN
PIGMENTARY DILUTION OF THE SKIN AND HAIR, THE PRESENCE OF LARGE
CLUMPS OF PIGMENT IN HAIR SHAFTS, AND AN ACCUMULATION OF
MELANOSOMES IN MELANOCYTES. MOST PATIENTS ALSO DEVELOP AN
UNCONTROLLED T LYMPHOCYTE AND MACROPHAGE ACTIVATION SYNDROME,
KNOWN AS HEMOPHAGOCYTIC SYNDROME, LEADING TO DEATH IN THE ABSENCE
OF BONE MARROW TRANSPLANTATION.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 DILUTE DOMAINS.
SIMILARITY: CONTAINS 1 DILUTE DOMAIN.
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MYOSIN HEAD-LIKE.

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IQ 2.
IQ 3.
IQ 4.
IQ 5.
IQ 6.
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COILED COIL (POTENTIAL).
DILUTE.
ATP (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
PHOSPHORYLATION (POTENTIAL).
MISSING (IN ISOFORM 2).
L -> LYFEELYADDPKKYQSYRISLYKRMI (IN
                                                                                                                                                                                                                                                                                                                                                                          Calmodulin-binding; Actin-binding; ; Alternative splicing; Polymorphism MYOSIN HEAD-LIKE.
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                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.
beta chain) (RNA polymerase beta subunit).
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                                                                                                                                                      [RNA](N).

SUBUNIT: THE ENZYME CONSISTS OF THE ENZYME WHICH IS COMPOSED OF 2 ALPHA BETA' CHAIN.
                                                                                                                             SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HETIQGV---SGVKPTGLRKRTSSIADEGTYTLDSILRQLNSFHSVMCQHGMDP--ELIK
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; 1C55AD57285FA9EC
                                                                                                                                         RNA POLYMERASE BETA CHAIN FAMILY.
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47;
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  http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                      CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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TISSUE SPECIFICITY: EXPRESSED IN BRAIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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RESULT 15
GP37_HUMA
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Best Local S
Matches 50
SEQUENCE FROM N.A.
JONES K., Tin WOllam A
Submitted (JUN-1998) t
-!- FUNCTION: ORPHAN R
-!- SUBCELLULAR LOCATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein-coupled library.";
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InterPro; IPRO1572; RNA_PO1_B.
Pfam; PF00562; RNA_PO1_B; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
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Marazziti D., Golini E., Gallo A., Lombardi M.S., Matteoni
Tocchini-valentini G.P.;
"Cloning of GPR37, a gene located on chromosome 7 encoding
"Crotein-coupled peptide receptor, from a human frontal br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                Su K., Kyaw H., Li Y.;
endothelin receptor type-B-like gene enriched
Blophys. Res. Commun. 233:559-567(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene encodes a putative G protein-coupled in the central nervous system."; d (AUG-1997) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45:68-77(1997).
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                                                                 m A., Keppler D.;
) to the EMBL/GenE
N RECEPTOR.
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                                                                                                         EMBL/GenBank/DDBJ databases
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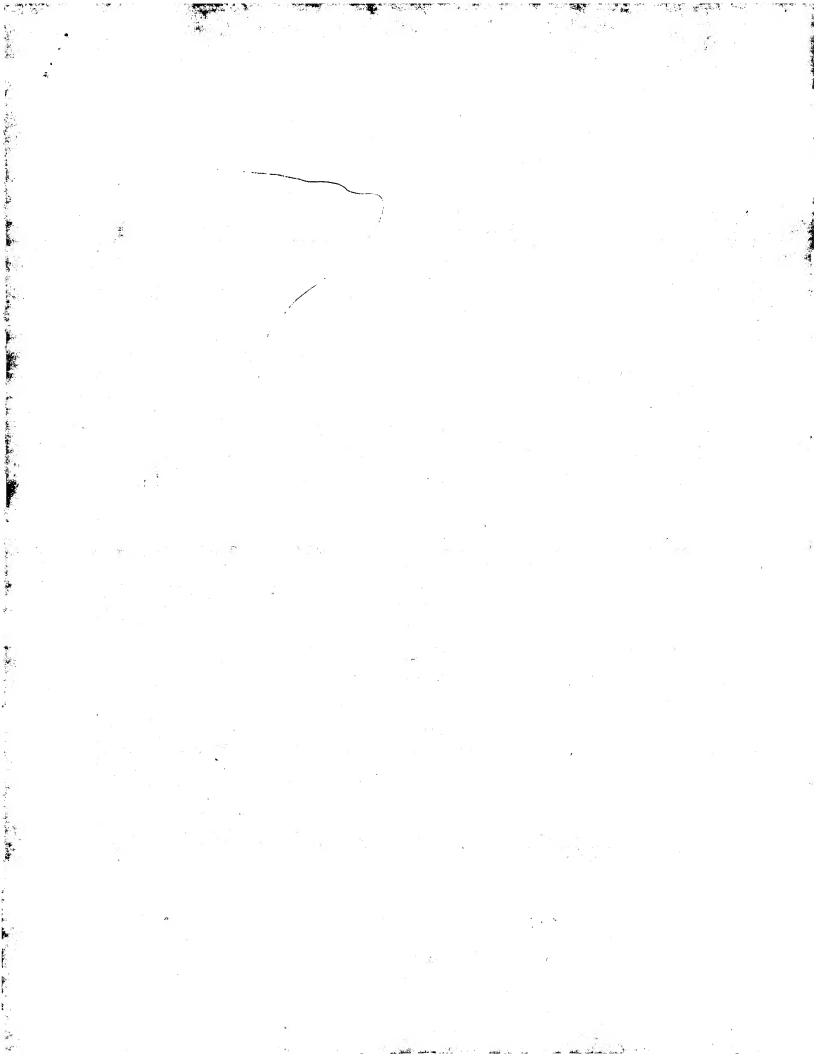
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EMBL;
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een the Swiss Institute of Bioinformatics and the EW
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ps00237; G_PROTEIN_RECEP_F1_1;
ps50262; G_PROTEIN_RECEP_F1_2;
ps50262; G_PROTEIN_RECEP_F1_2;
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Qy 84 LTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDR 123	Query Match 9.0%; Score 90.5; DB 2; Length 1056; Best Local Similarity 25.0%; Pred. No. 4; Matches 42; Conservative 23; Mismatches 52; Indels 51; Gaps 8; Qy 24 HPESILSDEDYWDYVVPEPNLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEK 83	ternate names: protein L1917; protein ecles: Saccharomyces cerevisiae te: 27-Aug-1995 #sequence_revision 19-cession: S56039; S64866 zuta, K. zuta, K. zuta to the EMBL Data Library, Decemb ference number: S56039 lecule type: DNA sidues: 1-1056 <niz> loss references: EMBL:D43895; NID:g6190 etter, P., Rose, M.; Entian, K.D. itted to the Protein Sequence Database ference number: S64866 lecule type: DNA sidues: 1-1056 <koe> sidues: 1-1056 <koe> sosr-references: EMBL:Z73211; NID:g1360 perimental source: strain S288C ne: SGD:RIC1 oss-references: SGD:S0004029; MIPS:YLR position: 12R position: 12R position: 12R</koe></koe></niz>	ALIGNMENTS 1	30 75.5 7.5 1603 2 D89407 protein R10E8.6 [1 31 75.5 7.5 1696 2 TZ4146 hypothetical protein R20E8.6 [1 32 75 7.5 1696 2 TZ4146 hypothetical protein R20E8.6 [1 32 75 7.5 1696 2 TZ4146 hypothetical protein R20E8.6 R2
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RESULT 2
730107
hypothetical protein F44C4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30107
C;Accession: T30107
C;Accession: T30107

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A;Description: The sequence of C. elegans cosmid T10H9
A;Reference number: 221306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T10H9.2 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33236
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A; Residues: 1-711 <GEI>
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                                                                                                                                                                                                                                      γo
                                                                                                                                                                                                                                                                                                                                                          A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF067949; PIDN:AAC19236.1; GSPDB:GN00023; CESP:T10H9. A;Experimental source: strain Bristol N2; clone T10H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDB:
A;Molecule type: DNA
A;Residues: 1-1414 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T33236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDB
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                   160
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                                                                                                                                4:17
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                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.; Bradshaw, H.; O'Brien, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENCLSKSKQTKLGCSKVLV----PEKLTQRIAQDVL-RLSSTEPCG-----LRGCVM
                                                                                                                                                                                                        SDEMDCG-NINGTMCDFNGQDYCNSWYQVTNVTDYHERLSEPTTVAPLNKLNEVPLHLFR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFYLCSRTYSKVWQISVISKGINPMESGRTIIYEAGYTLIPK-ENCTW----ERVFVNIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVNL-----EIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDEMDCG-NINGTMCDFNGQDYCNSWYQVTNVTDYHERLSEPTTVAPLNKLNEVPLHLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELLDCGYHPESLLSDF----DY---WDYVVPEPNLNEVIFEESTCQNLVKM------
                   FSSGFRRTLILSSGF
                                                                                         HVNL-----EIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGR 159
                                                                                                                              LQSPSAKIKEAMRGSGNMLVFDHKPNPLTRRTSALVSPELPRTNPEAYDEKSPLFKSCKL
                                                                                                                                                                   LENCLSKSKQTKLGCSKVLV----PEKLTQRIAQDVL-RLSSTEPCG------LRGCVM
                                                                                                                                                                                                                                         SELLDCGYHPESLLSDF----DY----WDYVVPEPNLNEVIFEESTCQNLVKM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQSPSAKIKEAMRGSGNMLVFDHKPNPLTRRTSALVSPELPRTNPEAYDEKSPLFKSCKL
                                                        RFYLCSRTYSKVWQISVISKGINPMESGRTIIYEAGYTLIPK-ENCTW---ERVFVNIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3; 520/2;
                                                                                                                                                                                                                                                                                                                                                       56/3; 76/1; 101/1; 161/1; 196/1; 226/3; 269/2; 318/1; 364/1; 475/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46;
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                              8.5%; Score 85.5; I
23.6%; Pred. No. 16;
tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
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Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                   Length 1414;
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                                                                                                                                                                                                                                                                                Indels
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C; Genetics:
A; Gene: CAC2581
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745
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DLMKYKITYLS
                                                                          YKLCFENADSYIFHKSTPKAFGVITKYEGLCIGKSAKEIQLLYPSFKIGSSNNLEDYSLN 744
                                                                                                                                                  GAATSSNIVLLNTALENGYYKYMFDRSLEMGCDTVVLRKSVIKDNRKSFSDIDYGAKLSG 684
                                                                                                                                                                                     GSLSSKNPASISELLDCGYHP--------
                                     QRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLD----RIVCDSSVVPTFELT----
                                                                                                           YVVPEPNLNEVIFEESTCQN----LVKMLENCLSKSKQT------KLGCSKVLVPEKLT 85
                                                                                                                                                                                                                                           Similarity
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Conservative

40;

----ESLLSDFDYW----D

-GFSYNNRSKAEGIVKKLSKKGVRVIVDMNRIPTDNITDRMI 796

8.2%; 19.0%;

Score 82; Pred. No. Mismatches

DB . 23; 2;

Length 1002;

Indels

82;

Gaps

10;

PID:915025604; GSPDB:GN00168 ATCC824

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A; Delaws: r--- DNA
A; Molecule type: DNA
A; Residues: 1-673 <STO>
A; Cross-references: GB:chr_V; PIDN:AAC27338.1; PID:g3335245; GSPDB:GN00023; CESP:F25E
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1002 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK80530.1;
A;Experimental source: Clostridium acetobutylicum
                                                                                                                                                                R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: F89101
                                                                                                                                                                                                                                                                                                          C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: G97217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: F89101
R;anonymous, The C. elegans Sequencing Consortium
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein F25E5.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                      A; Reference number: A; Accession: G97217
                                                                                                                                                                                                                                                                                                                                                                                             conserved membrane protein CAC2581 (6-pyruvoyl-tetrahydropterin synthase related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: F25E5.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 STCQNLV--KMLENCLSKSKQTKLGCS-----KVLVPEKLTQRIAQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VATGSLSSKNPASISEL------LDCGYHPESLLSDFDYWDYVVPEPNLN--EVIFEE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCQNVILEDLNENKLSTKNKTKLAESYDLDTVRELFNPNTMTQPSAR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNAGERIGIEVTNYE
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29; Conserv
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26.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                   Zeng,
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                                                                                                                                                                                                                                                                                   Gibson,
                                                                                                                                                                                                   Bacterium
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                                                                                                                                                                                                                                                                                   R.;
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ο Σ	nes 41; Conservative 18; F.EG. NO. 32; 10 KNPASISELLDCGYPESLLSDFDYWDYVPEPNLNEVIFEESTCONLV- 58 1	Matches Qy 10 F	
a C a a a a a a a a a a a a a a a a a a	al source: brain 10685 10685	A; Experimenta C; Genetics: A; Note: KIAAO Query Match	
A; A A; S	3U	A: ACCESSION: TOOS A: Status: prelimin A: Status: prelimin A: Molecule type: r A: Residues: 1-927	
gas DNA A;T	of the coding sequences of unidentified human genes. X. The comple 214142; MUID:98403880	DNA Res. 5, 169-176 A; Title: Prediction A; Reference number:	
RES hyp C;S C;A	RESULT 7 TO0357 hypothetical protein KIAA0685 - human hypothetical protein KIAA0685 - human C;Species: Homo sapiens (man) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000 C;Accession: T00357 C;Accession: T00357 R;Jshikawa, K.; Nadase, T.; Suyama, M.; Miyaiima, N.; Tanaka, A.; Kotani, H.; Nomura, N.	RESULT 7 T00357 hypothetical protei C;Species: Homo sap C;Date: 01-Feb-1999 C;Accession: T00357 R;Ishikawa, K; Naq	
Оу	SGPRLVKKKLYSLIGT 187 : : :: :: ADPPITEEELNKILST 120	Oy 172 9	
Qy Db	LEIENVCKKLDRIVCDSSVVPTFELTLVFKOENCSWTSFRDFFFSRGRFSSGFRRTLILS 171	Oy 112 I	
Qy	TCONLVKMLENCLSKSKQTKLGCSKVLVPE-KLTQRIAQDVLRLSSTEPCGLRGCVMHVN 111 : : :	Oy 53 :	
X B O	tch 8.1%; Score 81.5; DB 2; Length 228; al Similarity 22.8%; Pred. No. 4.2; 31; Conservative 24; Mismatches 48; Indels 33; Gaps 5;	Query Match Best Local Matches 3	
A;GGEGR	Status: preliminary Molecule type: DNA Residues: 1-228 <kur> Cross-references: GB:AE006641; NID:g13814569; PIDN:AAK41593.1; GSPDB:GN00155 Genetics: Genetics: SSO1357</kur>	A;Status: prelimina A;Molecule type: DN A;Residues: 1-228 < A;Cross-references: C;Genetics: A;Gene: SSO1357	
A	Description: Sulfolobus solfataricus complete genome. Reference number: A99139 Accession: B90292	A; Description: Sulfa A; Reference number: A; Accession: B90292	
R; I ili Nat	<pre>K;SNe, Q.; Singn, K.K.; Contalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan- Jong, I.; Jefffles, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001</pre>	Jong, I.; arrett, R.! submitted 1	
D85 hyp C;S C;D C;A	protein SSO1357 [imported] - Sulfolobus solfataricus ulfolobus solfataricus ny-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 1890292	B90292 hypothetical C; Species: Si C; Date: 24-M C; Accession:	
R F.S	INDKKIAFLASGI 863	RESULT 6	
Qy		177	
Db S	GVISEPIVEDNKMPDLFENKERYVADVKFKBEYKKWNTVYLTNTQNVKGFSW	797	
Qy	LVFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRL 176	Оу 138	

```
hypothetical protein 20521 [imported] - Escherichia coli (strain O157:H7, substrain E. C;Species: Escherichia coli
C;Bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85538
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda-Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Roccession: D85538
A;Status: preliminary
A:Molecule type. Num
                                                                                                                                                                                                                                                                           R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Cgasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Hitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gla;Pittle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gla;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90687
                                                                                                                                                   A;Cross-references: GB:BA000007; PIDN:BAB33895.1; PID:g13359929; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                      \;Molecule type: DNA
\;Residues: 1-523 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ECs0472 [imported] - Escherichia coli (strain 0157:H7, substrain 7.5pecies: Escherichia coli 7.5pecies: Escherichia coli 7.5pecies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 7.4ccession: H90687
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A;Residues: 1-523 <STO>
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                                                                                                                                                                                                                                                      ;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N:Cross-references: GB:AE005174; NID:g12513274; PIDN:AAG54768.1; GSPDB:GN00145; UWGP:
N:Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 40; Conserv
     Matches
                                Best
                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 KLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YNSTIKHNIIFYKDGENLMIRGTISIVNEVVKTYSLPIEKDDNGYYDFSGLYLAHSNISG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSVLNYNSALTPDPNFN--IDATSDLDSYLKLDFDRLSPKQKQTTLCCFWNKIASSLPEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 LSDFDYWDYVVPEPNLNEVIFEESTCQNLVKMLENCLS-KSKQTKLGC--SKVL--VPEK 83
                                                                                                        ECs0472
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     40;
                          Similarity
  Conservative
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                        7.9%; Score 79.5;
24.5%; Pred. No. 18;
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  24;
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Pred. No. 18;
24; Mismatches
  Mismatches
                                                     DB
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  62;
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                                                Length 523;
  Indels
  37;
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Gaps
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  7;
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29 LSDFDYWDYVVPEPNLNEVIFEESTCQNIVKMLENCLS-KSKQTKLGC--SKVL--VPEK 83

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A;Cross-references: EMBL:U21324; NID:g687879; A;Experimental source: strain Bristol N2 R;Yuan, J.; Horvitz, H.R.
                                                                                                                                                                                                                                                                                          RESULT 11
S72566
cell death
                                                                               A:Authors: Shownkeen, R.; Smal
proat, J.; Wohldman, P.
A;Description: The C. elegans
A;Reference number: $72566
A;Accession: $72566
                                                                                                                                                                           cell death protein ced-4 - Caenorhabditis elegans
(Alternate names: hypothetical protein C35D10.9
C;Species: Caenorhabditis elegans
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 31-oct-1997
C;Accession: S72566; A49152
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.;
ulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jöhnston,
B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders,
C; Rifken, L.; Roopra, A.; Saunders,
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JW0054
                                                   A; Molecule type: DNA
A; Residues: 1-549 <WIL>
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A;Introns: 91/2 179/2 349/3 396/2 439/3 520/2
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C;Genetics:
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A; Residues: 1-606 < DAR>
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A;Title: A new member of the amiloride-sensitive sodium channel family in Drosophila me.
A;Reference number: JW0054; MUID:98262943
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Best Local S
Matches 35
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                                                                                                                                             R.; Smaldon,
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19.3%;
                                                                                                                  genome
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                                                                                                                                                  N.; Smith,
                                                                                                                                                                  February 1995
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                                                                                                                project: Contiguous nucleotide
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                                                                                                                                                Α.,
                                  PID: 9687887
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                                                                                                                                                Sonnhammer, E.;
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                                                                                                                                                Staden,
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Saunders,
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A; Introns: 151/1;
                   δÃ
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A;Note: Anabaena sp. (strain PCC /140/ 2001 #tex C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #tex C;Accession: AB1847
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sas R;Kaneko, T.; Nakamura, S.; Sugimoto, M.; Takazawa, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status, rank A; Shalus Richard Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A49152; MUID:93161939
A;Accession: A49152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuna Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Reference number: AB1807; MUID:21895285; PMID:11759840
A; Accession: AB1847
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A; Residues: 1-211,213-549 <YU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 NPASISELLDCGYHPESLLSDF--DYWDYVVPEPNLNEVIFEESTCONLVKMLENCLSKS
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                                                                                                      ANELDDALQSSLILPLNETYRIPLLFHSQD-
                                                                                                                                                                              CKKLDRIVCDSSVVP---TFELTLVFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGF
                                                                                                                                                                                                                                                                                                                                                                                                          NPFFINQLLKALYQESLLIFDFTTQKWQW----
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                                                                                                                                                                                                                                                          SVVELVSSRIQLLPEK-TQKILQ-
                                                                                                                                                                                                                                                                                                                              KQTKLGCSKV-LVPEKLTQRIAQDVLRLSSTEPCGLRGCV-----MHV-----NLEIENV
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Pred. No.
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Pred. No.
                                     193
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14-Dec-2001 #text_change 11
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M.; Yamada,
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A;Gene: LON2
A;Gene: LON2
C;Function:
A;Description: Serine proteinase
A;Description: AFP-dependent serine proteinase La
C;Superfamily: ATP-dependent serine proteinase La
C;Keywords: ATP; DNA binding; hydrolase; mitochondrial matrix;
F;455-462/Region: nucleotide-binding motif A (P-loop)
F;318-523/Region: nucleotide-binding motif B
F;461/Binding site: ATP (Lys) #status predicted
T-0463/Active site: Ser #status predicted
                                                                                                                                                                                                                                            A; MoLecule type: mRNA
A; Residues: 1-964 <BAR>
A; Cross-references: EMBL: U85495; NID: g1816587; PIDN: AAC50021.1; PID: g1816588
A; Experimental source: strain B73
                                                                                                                                                                                                                                                                                                                                                              R;Barakat, S.; Pearce, D.A.; Sherman, F.; Ra
Plant Mol. Biol. 37, 141-154, 1998
A;Title: Maize contains a Lon protease gene
A;Reference number: 215282; MUID:98281582
                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable ATP-dependent proteinase LON2 (EC 3.4.21.-), mitochondrial - maize
C;Speciles: Zea mays (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Jan-2001
C;Accession: T04325
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C;Superfamily: starch synthase
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A;Cross-references: GB:AE000704; NID:g2983301; PIDN:AAC06894.1; PID:g2983303; GB:AE00065
A;Experimental source: strain VF5
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C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
C:Accession: C70363
                                                                                                                                                                                                                           C; Genetics:
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Matches 37
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Search completed: October 11, Job time : 52 secs
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A; Residues: 1-817 <STO>
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ALIGNMENTS

AAY59820 ID AAY59820 standard; Protein; 177 AA. XX AC AAY59820;
9820 standard; Protein; 177 AA. 9820; IAN-2000 (first entry) In normal ovarian tissue derived protein 97. In; ovary; screening; ovarian cancer; treatment. 9 sapiens. 9816395-A1. CCT-1999. PR-1998; 98DE-1016395. PR
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Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel nucleic acid sequences that are highly expressed in normal ovary tissue. Artificial chromosomes and cosmid clones containing the sequences can be used as gene transfer vehicles. The sequences can be used to produce DNA fragments containing full-length genes. Host cells transformed with the sequences can be us
Sequences AAY03632-36 the invention. The ger
                                          Claim 14; Page 82-83; 92pp; English.
                                                                                    New isolated hypoxia-related use in therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY03635;
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(QUAR-) QUARK BIOTECH INC
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                                                                                    genes
in e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
products of eir products
                                                                                    e.g. hypoxia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272.5;
No. 9.
                                                                                     used to develop products
hypoxia, ischaemia, apopto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
 hypoxia-regulated genes of can be used therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                    reattachment;
                                                                                     apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 3
AAE03922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and diagnostically in hypoxia, ischemia, apoptosis and angiogenesis. products and methods can be used for e.g. inducing apoptosis in tumorigenic cells or angiogenesis in trauma situations where e.g. a l must be reattached or in a transplant where revascularisation is need
           Nucleic acids encoding 50 human secreted polypeptides, preventing, diagnosing and/or treating diseases, e.g. \mid disease, botulism, cancers and Scimitar syndrome -
                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                          endocrine disorder; infection; wound hea
cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                              11-JUN-1999;
                                                                                                                                                                                       01-JUN-2000; 2000WO-US15136
                                                                                                                                                                                                                21-DEC-2000
                                                                                                                                                                                                                                           WO200077022-A1.
                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               binding
                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorder; pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE03922 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCDSSVVPTFELTLVFKQENCSWTSFRDFFFS-RGRFSSGFRRTLILSSGFRLVKKKLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAQARLGSRRPARLIMPSQLVSQVGKELLRLAYSEPCGLRGALLDVCVEQGKSCHSVGQL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLESSDCESL-DSSNSGFGPE---EDTAYLDGVSLPDFELLSDPEDEHLCANLMQLLQES 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSSKNPASISELLDCGYHPESLLSDFDYWDYV-VPEPNLNEVIFEESTCQNLVKMLENC
                                                                              2001-367020/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDPSLVPTFQLTLVLRLDSRLWPKIQGLFSSANSPFLPGFSQSLTLSTGFRVIKKKLYS
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                                                                                                          CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  secreted protein;
                                                                   AAD08369
                                                                                                                                                                                                                                                                                                                                                                             partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
                                                                                                          Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 encoded secreted protein HUKCS86, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                              99US-0138629
                                                                                                                                                                                                                                                                                                                                                                               identification
                                                                                                                                                                                                                                                                                  /label= signal_peptide
22..232
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                          ,MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%;
35.0%;
                                                                                                           Komatsoulis
                                                                                                                                                                                                                                                                     "Mature secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271; DB 20;
No. 2.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                        healing;
                                                                                                                                                                                                                                                                                                                                                                                           gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary;
                  e.g. Parkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO:85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour;
                            on's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Claim 11; Page 538-539; 614pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                       Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 50 genes, based on the tissues in which they are most highly expressed,
                                                                                                                                          cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperpoliferative disorder; cardiovascular disorder; angiogenesis;
                                                                                                                             cerebrovascular disorder; nervous system disorder;
                                                                                                                                                                                                                                                                              Human secreted
                                                                                                                                                                                                                                                                                                                      26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                     AAB51661 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The genes and their secreted protecting or ameliorating medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein genes and
AAE03948-AAE03996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDPSLVPTFQLTLVLRLDSRLWPKIQGLFSSANSPFLPGFSQSLTLSTGFRVIKKKLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCDSSVVPTFELTLVFKQENCSWTSFRDFFFS-RGRFSSGFRRTLILSSGFRLVKKKLYS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLESSDCESL-DSSNSGFGPE---EDTAYLDGVSLPDFELLSDPEDEHLCANLMQLLQES 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAQARLGSRRPARLLMPSQLVSQVGKELLRLAYSEPCGLRGALLDVCVEQGKSCHSVGQL
                                                                                                    healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or ameliorating medical conditions, e.g., by protein or Pathological conditions can be diagnosed by determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               their secreted proteins are useful for preventing
                                                                                                                                                                                                                                                                       protein sequence encoded by gene 42 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                      skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represent cDNAs corresponding to 50 numeur section.
AAE03898-AAE03947 represent the proteins they encode.
Thoman secreted protein fragments or variants.
                                                                                                    aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.0%;
35.0%;
                                                                                                      food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 271; DB 22;
Pred. No. 2.1e-22;
5; Mismatches 66
                                                                                                      additive;
                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                          NO:101.
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ophthalmological. The polynucleotides and polypeptides can be used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a CC pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardicvascular CC disorders, infections caused by bacteria, viruses and fungi and ocular CC disorders, infections caused by bacteria, viruses and fungi and ocular CC disorders. The polypeptides can also be used to aid wound healing and CC epithelial cell proliferation, to prevent skin aging due to sunburn, to CC maintain organs before transplantation, for supporting cell culture of CC polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC93355 to AAC93363 and CAAB51619 represent sequences which are used in the exemplification of the
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention. Human secreted protefus have qualified activities include: and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; cytostatic; cardiant; vasotropic; cerebroprotective; and neuroprotective; antibacterial; virucide; fungicide; and neuroprotective; antibacterial; virucide; fungicide; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human secreted proteins given in AAB51b2u to Ambarava proteins AAB51722 represent human secreted polypeptide sequences and proteins 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polynucleotide sequences given in AAC93364 to AAC93412 encode human secreted proteins given in AAB51620 to AAB51668. AAB51669 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 486-487; 540pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC93405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JAN-2000;
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SLESSDCESL-DSSNSGFGPE---EDTAYLDGVSLPDFELLSDPEDEHLCANLMQLLQES 103
                                                                                                               SLSSKNPASISELLDCGYHPESLLSDFDYWDYV-VPEPNLNEVIFEESTCQNLVKMLENC 64
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Pred. No. 2.1e-22;
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                                                                                                                                                                                                                                                                                                                                                     Length 233;
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RESULT 5
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                                                                                                                                                          ALDPSLVPTFQLTLVLRLDSRLWPKIQGLFSSANSPFLPGFSQSLTLSTGFRVIKKKLYS
                                                                                                                                                                                            VCDSSVVPTFELTLVFKQENCSWTSFRDFFFS-RGRFSSGFRRTLILSSGFRLVKKKLYS
                                                                                                                                                                                                                                                               LSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCGLRGCVMHVNLEIENVCKKLDRI 124
                                                                                                                                                                                                                              LAQARLGSRRPARLLMPSQLVSQVGKELLRLAYSEPCGLRGALLDVCVEQGKSCHSVGQL
(first entry)
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RESULT 6
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAY03632-36 represent products of hypoxia-regulated genes of the invention. The genes and their products can be used therapeutically and diagnostically in hypoxia, ischemia, apoptosis and angiogenesis. The products and methods can be used for e.g. inducing apoptosis in tumorigenic cells or angiogenesis in trauma situations where e.g. a limb must be reattached or in a transplant where revascularisation is needed.
                           pharmaceutical
                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                       Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                   ABB63344;
                                                                                                                                                                                                                                                                     ABB63344 standard;
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                                                                                                                                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                      189 LLSSANSSLVPGYSQSLTLSTGFRVIKKKLYS 220
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DB; AAX29137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFFS-RGRFSSGFRRTLILSSGFRLVKKKLYS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRLSSTEPCGLRGCVMHVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YWDYY-VPEPNLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLTQRIAQDV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGSLSSKNPA-----GYHPESLLSDFD 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRLAYSEPCGLRGALLDVCVEQGKSCHSVAQLALDPSLVPTFQLTLVLRLDSRLWPKIQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 AA;
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angiogenesis; tumorigenic cell; trauma; limb reattachment;
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                                                                                                                                                              (first entry)
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Pred. No. 2.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes - used to develop products for in e.g. hypoxia, ischaemia, apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                         ID NO 16824
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RESULT 7
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Matches 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic agenes from Drosophila interactions -
                                                                                                      Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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11-JUL-2000; 2000US-0614150
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                                                                      pharmaceutical.
                                                                                 Drosophila;
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                                                                                                                                                         АВВ63379;
                                                                                                                                                                                ABB63379 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ
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                                                                                                                                                                                                                                                                                                                                        162 NLDDV--SASAVRELSQQLQAQLRDAKRRHLACTEVTLPNDLTQRIAAEIIRMSEREPCG 219
                                                                                                                                                                                                                                                                                                                                                       43 NLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLTQRIAQDVLRLSSTEPCG 102
                                                                                                                                                                                                                                                                                                        LRGCVMHVNLEIE-NVCKKLDRIVCDSSVVPTFELTLVFKQENCSWTSFRDFFFSRGRFS 161
                                                                                                                                                                                                                                                                   SGFRRTLILSSGFRLVKKKLYS 183
                                                                                                                                                                                                                                                                                           ERACTLFIEFESEPNKVKRIAYFKVDPDTVSIFELYLTLRQDKSGWSSLVPQFIKNLTRS
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                                                                                 developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AA:
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                                                                                 biology;
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                                                                                                                                                                                                                                                                                                                                                                                       ; Score 211.5; DB 2; Pred. No. 1.7e-15; 24; Mismatches 60
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                                                                                 signalling; insecticide;
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WO200171042-A2

Drosophila melanogaster

27-SEP-2001

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RRESULT 8
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                                                                                                                                                                                             Human; secreted protein; immunosuppressive; antiarthritic; antirheumati antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; cancer; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The inventuation of the control of the control of the developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ABB57737-ABB72072). The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct
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                              05-OCT-2000
                                                                           WO200058467-A1
                                                                                                                           Homo sapiens
                                                                                                                                                                           nervous
                                                                                                                                                                                                                                                                                                                                        Human secreted protein sequence encoded by gene
                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB45148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB45148 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 16929; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFKQENCSWTSFRDFFFSRGRFSSGFRRTLILSSGFRLVKKKLYSLIG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPCDLTPSVAREIIRVSEKEPRGIRGCTIYIEFEDEPKNSRRIASIKVDSDTVSTFEVYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNSNYYYYAADEEEGGSADYALSNYDKKAVEELS----LRLLDE-LRAAKSRHLTCTEVS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-656860/75
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49; Conserv
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                                                                                                                                                                         system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AA;
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2000US-0614150
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                                                                                                                                                                         aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting for elucidating cell signalling
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Pred. No. 2e-13;
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                                                                                                                                                                                                                                                                                             antirheumatic;
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RESULT 9
ABB64251
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Drosophila; developmental biology; cell signalling; insecticide;

WO200171042-A2 Drosophila pharmaceutical

melanogaster

Drosophila melanogaster polypeptide SEQ ID NO 19545

ABB64251;

ABB64251 standard; Protein; 1066 AA

13

TFQLTLVLRLDSRLWPKIQGLFSSANSPFLPGFSQSLTLSTGFRVIKKKLYS

64

26-MAR-2002

(first entry)

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Query Match
Best Local
                                         Matches
                                                                                                                                                                                  system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC80522-C80530 and AAB45119 represent sequences used in the isolation and characterisation of the genes and proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequences AAC80531-C80580 represent cDNA encoding human secreted proteins AAB45120-B45195. Sequences AAB45170-B4525 represent alternative polypeptides encoded by the genes, and amino acid sequences to which they are homologous. The genes and proteins have activities dependent on the tissues and cells in which they are expressed. Examples of their activities include immunosuppressive; antiarthritic; cerebroprotective; notropic; neuroprotective; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and opthalmalogical. The secreted proteins, polynucleotides, antagonists and agonists may be useful in treating, preventing and/or diseases and diseases and diseases and diseases and diseases and diseases and diseases.
                                                                                                                                                                                                                                                                                                                                                                       e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 391-392; 440pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's Parkinson's diseases and cancers -
                                                                                                                         Sequence
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17-DEC-1999;
                                                                                                                                                                   the invention.
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133 TFELTLVFKQENCSWTSFRDFFFS-RGRFSSGFRRTLILSSGFRLVKKKLYS
                                                         Local
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                                                           Similarity
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                                                                                                                         74
                                         Conservative
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99US-0172410
                                                         11.28;
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                                         10;
                                                           Score 112.5; DB 2
Pred. No. 4.6e-05;
                                         Mismatches
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RESULT 10
AAB60490
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
21-JUL-1999;
08-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 discloses
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11-JUL-2000;
                                                                01-FEB-2001
                                                                                         WO200107471-A2
                                                                                                                                                        cell proliferative disorder; cancer arteriosclerosis; asthma; allergy;
                                                                                                                                                                                Cell cycle and proliferation protein; CCYPR; human antagonist; gene therapy; detection; gene therapy; transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder;
                                                                                                                                                                                                                                                   Human cell cycle and proliferation protein CCYPR-38,
                                                                                                                                                                                                                                                                                                                                AAB60490 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                      21-JUL-2000; 2000WO-US19948
                                                                                                                     HOMO
                                                                                                                                             menstrual cycle disorder; bacterial infection
                                                                                                                                                                                                                                                                               24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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2000US-0614150
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99US-0145075
99US-0153129
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25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred.
                                                                                                                                                                        cancer;
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                                                                                                                                                        r; tumour; anaemia; diabetes mellitus;
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                                                                                                                                                                                                                         human;
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                                                                                                                                                                                                                          agonist;
                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                        epilepsy
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Query Match
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Matches 53
                                                                                                                                                                                                                                                                   nucleotides can be used to generate transgenic animal models of human disease, and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR for the treatment or prevention of a disorder associated with CCYPR. Diseases which can be diagnosed, treated and prevented using CCYPR proteins, nucleic acids, agonists or antagonists include immune, developmental and cell signalling disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             overexpression of functional CCYPR. Monoclonal or polyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunoasays to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation proteins (CCYPR), which are encoded by AAF59500-AAF59643. CCYPR and agonists of CCYPR are used to treat diseases or conditions associated with decreased expression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with
                                                                                                                                                                                            disorders including cancer. Specific examples of these disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, allergies, diabetes mellitus, disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 146-148; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signaling disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillman JL,
Azimzai Y,
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAB60453-AAB60506 represent 54 human cell cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used to treat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-112727/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell cycle and proliferation proteins and polynucleotides to treat, diagnose and prevent immune, developmental and co
                                                                                                                                                                  γď
     Similarity 53; Conser
                                                                                                                                                                     bacteria
                                                                                                               934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang
     Conservative
                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0164647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT,
Lu DAM,
                               8.2%;
        29;
  Score 82; DB:
Pred. No. 4.7;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yue H,
Baughn N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Au-Young J,
R, Patterson
                                  DB
4.7;
                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders including cancer
        75;
                                                      Length 934;
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandman
C, Shah
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        Gaps
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RESULT 11
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                                                         26-JUN-2001
                                                                                       AAB92900
                                                                                                                     AAB92900 standard; Protein; 498
                                                                                                                                                                                             252 LLKNMF-----
                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                      134
                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                            10 KNPASISELLDCGY------HPESLLSDFDYWDYVVPEPNLNEVI--FEESTCQNLV-
                                                                                                                                                                                                                             SFRDFFFSRGRFSSGFRRTLILSSGFRLV
                                                                                                                                                                                                                                                                                         CKKLDRIV-----
                                                                                                                                                                                                                                                                                                                      RKTEQVITELKKKDKFISLVL-KHIGTSALMDLLLRLVSCVEPAGLRQDVLHW-LNEEKV
                                                                                                                                                                                                                                                                                                                                                  KMLENCLSKSKQTKLGCSKVLVPEKLTQRIAQDVLRL-SSTEPCGLRGCVMHVNLEIENV 117
                                                                                                                                                                                                                                                                                                                                                                                 KYPNTACELLTCDVPQISDRLGGDESLLSLL--YDFLDHEPPLNPLLASFFSKTIGNLIA 133
                                                                                                                                                                                                                                                             IQRLVELIHPSQDEDRQSNASQTLCDIVRLGRDQGSQLQEALEPDPLLTALESRQDCVEQ
                                                         (first entry)
                                                                                                                                                                                                -DGDRTESCLVSGTQVL
                                                                                                                                                                                                                                                                                         -----CD------SSVVPTFELTLVFKQENCSWT 148
                                                                                                                     A
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Human

protein

sequence SEQ

ID NO:11520.

primer;

detection;

diagnosis; antisense therapy; gene therapy

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                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC composition of a polynucleotide specification, where the CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary to a polynucleotide comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC complementary to a polynucleotide comprises a 3'-end sequence, where the CC complementary for comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers set useful for synthesising polynucleotides, CC useful and comprises are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC NAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13637 to AAH18742 represent human colon sequences; and AAH13637 to AAH13632.
                                                                                                                                                                                                            Best
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                         Query Match
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                 AAB95893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
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27-AUG-1999;
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                                                   406
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                                                   LEKQAYYLTYILLHLVGEVSCSHS:
                                                                                                                                             NIMKNIRDWNTKVPELCLGINELSSHPHNILWIVQLVPNWTSRGRCLR-QCLSLVIISKL
                                                                                                                                                                       SLLSDFDYWDYVVPE--PNLNEVIFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKL
                                                                                                  LDEKHEDVPNASN-
                                                                                                                       TQRIAQDVLRLSSTEPCGLRGCVMH----VNLEIENVCKKL------DRIVCDS---- 128
                                                                                                                                                                                                  . Similarity 39; Conserv
                                                                                                                                                                                                                                                                        present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                       -SVVPTFELTLVFKQENCSWTSFRDFFFSRGRFSSGFRRTLII.SSG
                                                                                                                                                                                                                                                                                              represent human amino acid sequences; and AAH13629 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID 11520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                ΑA;
                                                                                                                                                                                                                                                                        invention.
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T, Wakama
                                                                                                                                                                                                           8.0%;
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                                                                                                LQVSVLHRYLVQMKPSDLLKKMVLKKKAEQPDGIIDDSLHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu
                                                                                                                                                                                              33;
                                                                                                                                                                                              Score 80.5; DE Pred. No. 2.9; 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K,
A, Nagai K,
                                                ---FSSGQRKHFVLLCG 443
                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K,
Otsuki
                                                                                                                                                                                                                      22;
                                                                                                                                                                                               58;
                                                                                                                                                                                                                     Length
                                                                                                                                                                                               Indels
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                                                                       173
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                                                                                                                                                                                                                       498;
                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                               AAH13632
                                                                                                                                                                                            Gaps
                                                                                                405
                                                                                                                                              350
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RESULT 13
AAM79768
ID AAM79
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                        Sequence
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RESULT 12 ABB59933

AAM79768 standard; Protein; 860

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capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 6591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
N-PSDB; ABL04036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB59933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB59933 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB57737-ABB72072)
I 169
                                    NCMPACTSLEYNFEISRAKYDVAKTIRAFREEYEHTDAIGSRLSVYFKEHQFTA-IKRTI
                                                                         D----SSVVPTFELTLVFKQENCSWTSFRD--
                                                                                                                  FWMPKPL-
                                                                                                                                        VLVPEKLTQRIAQDVLRLSSTEPCGLR--GCV-----MHVNLEIENVCKKLDR---IVC
                                                                                                                                                                                           YVVSTDNLHEITPEKRQCLFDDERSLRFFRSYSQSNCQT-----ECLANYTVSKCGCAK
                                                                                                                                                                                                                                  YVVPEPNLNEVI -----
                                                                                                                                                                                                                                                                       1 Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                                606 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental
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2000US-0614150
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                                                                                                                                                                                                                                                                                       7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ľ
                                                                                                              -GTPVCGLKDINCYTSAQDELYTLMQNQTMAKSIDESVDITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection reagent for detecting 1000 or for elucidating cell signalling and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biology;
                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                              -----FEESTCQNLVKMLENCLSKSKQTKLGCSK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606
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                                                                                                                                                                                                                                                                                       Score 79.5;
Pred. No. 4
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                                                                                                                                                                                                                                                                       ed. No. 4.9;
Mismatches
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                                                                                                                                                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                         22;
                                                                       FFFSRGRFSSGFRRTL
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insecticide;
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                                                                                                                                                                                                                                                                                                           606;
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he invention
qnalling and
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19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                        The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, because diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xue
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nervous system disorder; arthritis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001 (first entry)
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM79768;
 100
                                                                      646
                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5-SEP-2000;
                       706
                                                                                                                                                                                                       AAM80020) are omitted as the relevant pages
                                               48
                                                                                               N
PC---GLRGCVMHVNLEIENVCKKLDRIVCDSSVVPTFELTLVFKQENCSW---
                                                                       IKTGELLGFPVYASRKSIAIRNXNNDKWPPERIIQYYGPATXAQDGSWGYRIPIYMINRI 705
                                                                                               VATGSL----SSKNPASISELLDCGYHPESLLSDF-----
                                                                                                                                                                                           missing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-476283/51.
                                               IFEESTCQNLVKMLENCLSKSKQTKLGCSKVLVPEKLTQ-----RIAQDVLRLSSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                  Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                                                                                                                    : acids encoding polypeptides with cytokine-like activities,
in diagnosis and gene therapy -
                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang L.
                                                                                                                                                                                                                                                                                                                                                                            Page 327-328; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0496914
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-063261.
2000US-0663561.
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                                                                                                                                                                                                                                     encoding human secreted proteins (II) (I) and (II) are used to prevent, contents of ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with sequences may also be used as DNA probes in diagnostic assays (e.g. collapserase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immunofactorial arthitis
                                                                                    (human immunodeficiency virus) infections, anaemia, rheumatoid arthriti and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theumatoru at the transfer of the state of t
cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, virus fungi and ocular disorders (e.g. corneal infections). (I) an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions - \,
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rheumatoid arthritis; antiarteriosclerotic; cardiant; vascula;
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The sequences given in AAR53274-78 are encoded by mutant versions of the C. elegans ced-4 gene. A 2.2 kb mRNA was identified as the wild type ced-4 transcript. This transcript was present at normal levels in a ced-3 mutant, suggesting that ced-3 is not a transcriptional regulator of ced-4. The 2.2 kb transcript is primarily expressed during embryogenesis, which is consistent with observed cell deaths in C. elegans. The wild type Ced-4 protein is 549 amino acids in length and has a relative molecular mass of 62,877. Ced-4 is highly hydrophilic with
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                                                                                                                                                                                                                                                               Claim 10;
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                                                                                                                                                                                                                                                                                                                                   Sequence
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